

TABLE 1

15781	ttcattat	aatgaagt	aatgaagtat	ataacctttg	acacgtaagg	taacaatgtc
15841	gtcaactttc	attattatat	cactcctttc	taaaaaacgt	aaacgttata	cgtttcataa
15901	aatcctttat	gcatattcca	ttgttctatt	gggtcatcac	cagcaatata	agacaatatt
15961	gattctggtt	tagtttcgtt	gttttagttca	tcatttaaga	attgaacaac	agaactatta
16021	tagtttaata	atagttgttg	gcaagccgat	aataagttaa	ttgcattgtc	aaatgtataa
16081	gctggattcc	attgaatcag	tttattgaat	agttgcaaca	tttcagtata	ggcttgtcct
16141	ttttcttctg	gtgcattatc	aacattaacc	attattatca	cttcctaata	aagttgaaat
16201	tacgcgtaaa	acagaattat	gatttaaadc	ttcaatttca	tcaatgtcaa	catcataaaa
16261	tgaaatttca	ttttctgttc	tatcaaataa	cgctatacat	aaacttccat	tcttaaaaacg
16321	aaaaacatgc	ttcaactcaa	tgttttttgt	ttcattttcc	atttttggtta	ctccttggtt
16381	tgattacata	cttagtatag	caaacgttta	aaagttttgt	caatagtttt	tcttaaaaaa
16441	gttttaaataa	ttttaaaact	actatttaat	agaagaaata	agattttaag	ttcaaatacat
16501	aattttgaat	aaaagtcaat	agatacataa	attttgtatt	tgatgaatat	gtaataggtt
16561	agataagttg	gttaagttgt	tgacacagat	ttttaagttt	agtaaagaaa	tgataagtaa
16621	atttataagt	tttgatttgt	ataatcgttt	attttaaacc	ggtggggt	

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TABLE 2

1st position (5' end)	2nd position				3rd position (3' end)
	U	C	A	G	
U	Phe	Ser	Tyr	Cys	U
	Phe	Ser	Tyr	Cys	C
	Leu	Ser	Stop	Stop	A
	Leu	Ser	Stop	Trp	G
C	Leu	Pro	His	Arg	U
	Leu	Pro	His	Arg	C
	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
A	Ile	Thr	Asn	Ser	U
	Ile	Thr	Asn	Ser	C
	Ile	Thr	Lys	Arg	A
	Met	Thr	Lys	Arg	G
G	Val	Ala	Asp	Gly	U
	Val	Ala	Asp	Gly	C
	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

TABLE 3

44AHJDORF012, Nucleotides and amino acids sequences

```

8391 atgaacgaagtaaaattcagattttacagactcagaagcgtttcac
1   M N E V K F R F T D S E A F H
8436 atgtttatatacgctggggattttaaaattactctactttttattt
16  M F I Y A G D L K L L Y F L F
8481 gtattaatgttcggtgatattattacaggtatttcaaaagcaatt
31  V L M F V D I I T G I S K A I
8526 aaaaataataacttatgggtcaaaaaaatcaatgagaggattttct
46  K N N N L W S K K S M R G F S
8571 aaaaaattattgatattctgtattatcatttttagcaaacatcatt
61  K K L L I F C I I I L A N I I
8616 gaccagattttacaattaaaagggtggtctactcatgattacaata
76  D Q I L Q L K G G L L M I T I
8661 ttttattatattgcaaattgagggtactttctattgtagaaaattgt
91  F Y Y I A N E G L S I V E N C
8706 gcagaaatggacgtatttagtaccagaacaaattaaagataaatta
106 A E M D V L V P E Q I K D K L
8751 agagtcattaaaaatgatactgaaaagagtgataacaatgaacga
121 R V I K N D T E K S D N N E R
8796 tcaagagaagatagataa 8813
136 S R E D R *

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44AHJDORF025, Nucleotides and amino acids sequences

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15175 atggaacgtaaatatacaaaacggtattattatattgcatgagatt
1   M E R K Y K T V L L Y C D E I
15130 aaaggacattttccacatcaaattctcaatgtttgaagatttatat
16  K G H F P H Q I S M F E D L Y
15085 gacgctaaagttgtatattcatattatgaatataacctgttcact
31  D A K V V Y S Y Y E Y N L F T
15040 aaaaaatagcggtatatcatagaatacattaaggagatataa 14999
46  K K Y A Y I I E Y I K E I *

```

TABLE 4

Similarities with public sequences

Query= pt|110882 44AHJDORF012 44AHJD_NT|8391-8813|3 1
(140 letters)

Database: nr
445,337 sequences; 137,034,979 total letters

Sequences producing significant alignments:	Score (bits)	E Value
gi 140528 sp P24811 YQXH_BACSU HYPOTHETICAL 15.7 KD PROTEIN IN ...	80	6e-15
gi 4126631 dbj BAA36651.1 (AB016282) ORF45 (bacteriophage phi-...	76	1e-13
gi 141088 sp P26835 YNGD_CLOPE HYPOTHETICAL 14.9 KD PROTEIN IN ...	61	5e-09
gi 2293160 (AF008220) YtkC [Bacillus subtilis] >gi 2635548 emb ...	36	0.11
gi 1181973 emb CAA87743.1 (Z47794) holin protein (Bacteriophag...	31	3.8
gi 4981272 gb AAD35828.1 AE001744_18 (AE001744) carboxyl-termin...	30	8.5

Query= pt|110882 44AHJDORF012 44AHJD_NT|8391-8813|3 1
(140 letters)

Database: swissprot
83,367 sequences; 30,300,539 total letters

Sequences producing significant alignments:	Score (bits)	E Value
sp P24811 YQXH_BACSU HYPOTHETICAL 15.7 KD PROTEIN IN SPOIIC-C...	80	2e-15
sp P26835 YNGD_CLOPE HYPOTHETICAL 14.9 KD PROTEIN IN NAGH 3'RE...	61	1e-09
sp P18015 COP_CLOPE COPY NUMBER PROTEIN (ORF4).	28	7.9

Query= pt|110899 44AHJDORF025 44AHJD_NT|14999-15175|-3 1
(58 letters)

Database: nr
445,337 sequences; 137,034,979 total letters

Sequences producing significant alignments:	Score (bits)	E Value
gi 1706558 sp P52869 EAEA_HAFAL INTIMIN (OUTER MEMBRANE PROTEIN...	28	8.4

Query= pt|110899 44AHJDORF025 44AHJD_NT|14999-15175|-3 1
(58 letters)

Database: swissprot
83,367 sequences; 30,300,539 total letters

Sequences producing significant alignments:	Score (bits)	E Value
sp P52869 EAEA_HAFAL INTIMIN (OUTER MEMBRANE PROTEIN) (ATTACHI...	28	1.9
sp Q02785 PDR1_YEAST ATP-DEPENDENT PERMEASE PDR12.	27	4.2
sp P75252 Y350_MYCPN HYPOTHETICAL PROTEIN MG350 HOMOLOG.	27	5.6
sp P41665 Y112_NPVAC HYPOTHETICAL 10.5 KD PROTEIN IN HE65-PK2 ...	27	5.6
sp P26744 VG01_BPP22 PORTAL PROTEIN (PROTEIN GP1).	26	7.3
sp P36542 ATPG_HUMAN ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL P...	26	9.5
sp P35435 ATPG_RAT ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL (EC...	26	9.5

TABLE 5

Physico-chemical parameters for 44AHJDORF012

1 MNEVKFRFTD SEAFHMFIIYA GDLKLLYFLF VLMFVDIITG ISKAIKNNNL WSKKSMRGFS
 61 KKLLIFCIII LANIIDQILQ LKGGLLMIIT FYYIANEGLS IVENCAEMDV LVPEQIKDKL
 121 RVIKNDTEKS DNNERSREDR

Number of amino acids: 140
 Average molecular weight (Daltons): 16294.30
 Mean amino acid weight (Daltons): 116.39
 Monoisotopic molecular weight (Daltons): 16283.58
 Mean amino acid monoisotopic weight (Daltons): 116.31

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	6	4.29%	7.58%	Cys	C	2	1.43%	1.66%
Asp	D	9	6.43%	5.28%	Glu	E	9	6.43%	6.37%
Phe	F	10	7.14%	4.09%	Gly	G	6	4.29%	6.84%
His	H	1	0.71%	2.24%	Ile	I	18	12.86%	5.81%
Lys	K	13	9.29%	5.95%	Leu	L	16	11.43%	9.42%
Met	M	6	4.29%	2.37%	Asn	N	10	7.14%	4.45%
Pro	P	1	0.71%	4.9%	Gln	Q	3	2.14%	3.97%
Arg	R	6	4.29%	5.16%	Ser	S	8	5.71%	7.12%
Thr	T	4	2.86%	5.67%	Val	V	7	5.00%	6.58%
Trp	W	1	0.71%	1.23%	Tyr	Y	4	2.86%	3.18%

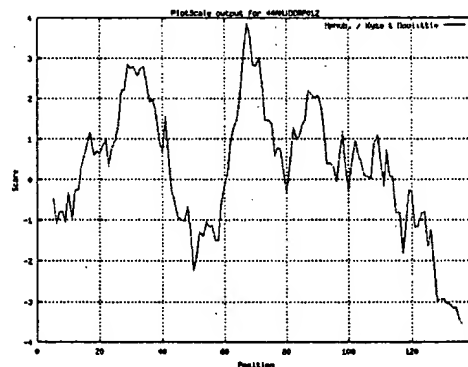
Number of acidic (negative) amino acids (ED): 18 12.86%
 Number of basic (positive) amino acids (KR): 19 13.57%
 Total charge (KRED): 37 26.43%
 Net charge (KR - ED): 1 0.71%
 Theoretical pI: 8.16
 Total linear charge density: 0.28

Average hydrophobicity: 1.26
 Ratio of hydrophilicity to hydrophobicity: 0.92
 Percentage of hydrophilic amino acid: 45.71%
 Percentage of hydrophobic amino acid: 54.29%
 Ratio of %hydrophilic to %hydrophobic: 0.84

Hydrophobicity plot

Kyte-Doolittle scale

Ala: 1.800 Arg: -4.500 Asn: -3.500
 Asp: -3.500 Cys: 2.500 Gly: -0.400
 Gln: -3.500 Glu: -3.500 His: -3.200
 Ile: 4.500 Leu: 3.800 Lys: -3.900
 Met: 1.900 Phe: 2.800 Pro: -1.600
 Ser: -0.800 Thr: -0.700 Trp: -0.900
 Tyr: -1.300 Val: 4.200



Physico-chemical parameters for 44AHJDORF025

1 MERKYKTVLL YCDEIKGHFP HQISMFEDLY DAKVVYSYYE YNLFTKKYAY IIEYIKEI

Number of amino acids: 58
 Average molecular weight (Daltons): 7248.41
 Mean amino acid weight (Daltons): 124.97
 Monoisotopic molecular weight (Daltons): 7243.60
 Mean amino acid monoisotopic weight (Daltons): 124.89

Amino acid composition

Acid	Symbol	Number	%	Average % in Swissprot	Acid	Symbol	Number	%	Average % in Swissprot
Ala	A	2	3.45%	7.58%	Cys	C	1	1.72%	1.66%
Asp	D	3	5.17%	5.28%	Glu	E	6	10.34%	6.37%
Phe	F	3	5.17%	4.09%	Gly	G	1	1.72%	6.84%
His	H	2	3.45%	2.24%	Ile	I	6	10.34%	5.81%
Lys	K	7	12.07%	5.95%	Leu	L	4	6.90%	9.42%
Met	M	2	3.45%	2.37%	Asn	N	1	1.72%	4.45%
Pro	P	1	1.72%	4.9%	Gln	Q	1	1.72%	3.97%
Arg	R	1	1.72%	5.16%	Ser	S	2	3.45%	7.12%
Thr	T	2	3.45%	5.67%	Val	V	3	5.17%	6.58%
Trp	W	0	0.00%	1.23%	Tyr	Y	10	17.24%	3.18%

Number of acidic (negative) amino acids (ED): 9 15.52%
 Number of basic (positive) amino acids (KR): 8 13.79%
 Total charge (KRED): 17 29.31%
 Net charge (KR - ED): -1 -1.72%
 Theoretical pI: 6.08
 Total linear charge density: 0.33

Average hydrophobicity: -3.72
 Ratio of hydrophilicity to hydrophobicity: 1.30
 Percentage of hydrophilic amino acid: 44.83%
 Percentage of hydrophobic amino acid: 55.17%
 Ratio of %hydrophilic to %hydrophobic: 0.81

Hydrophobicity plot

Kyte-Doolittle scale

Ala: 1.800 Arg: -4.500 Asn: -3.500
 Asp: -3.500 Cys: 2.500 Gly: -0.400
 Gln: -3.500 Glu: -3.500 His: -3.200
 Ile: 4.500 Leu: 3.800 Lys: -3.900
 Met: 1.900 Phe: 2.800 Pro: -1.600
 Ser: -0.800 Thr: -0.700 Trp: -0.900
 Tyr: -1.300 Val: 4.200

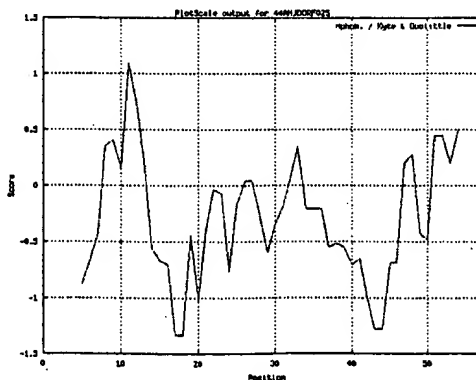


TABLE 6

>gi|11094395|gb|AAG29618.1| integrase-like protein [Staphylococcus aureus]
 >gi|11094394|gb|AAG29617.1|AF217235_20 Orf20 [Staphylococcus aureus]
 >gi|11094393|gb|AAG29616.1|AF217235_19 Orf19 [Staphylococcus aureus]
 >gi|11094392|gb|AAG29615.1|AF217235_18 Orf18 [Staphylococcus aureus]
 >gi|11094391|gb|AAG29614.1|AF217235_17 Orf17 [Staphylococcus aureus]
 >gi|11094390|gb|AAG29613.1|AF217235_16 Orf16 [Staphylococcus aureus]
 >gi|11094389|gb|AAG29612.1|AF217235_15 Orf15 [Staphylococcus aureus]
 >gi|11094388|gb|AAG29611.1|AF217235_14 Orf14 [Staphylococcus aureus]
 >gi|11094387|gb|AAG29610.1|AF217235_13 Orf13 [Staphylococcus aureus]
 >gi|11094386|gb|AAG29609.1|AF217235_12 Orf12 [Staphylococcus aureus]
 >gi|11094385|gb|AAG29608.1|AF217235_11 Orf11 [Staphylococcus aureus]
 >gi|11094384|gb|AAG29607.1|AF217235_10 Orf10 [Staphylococcus aureus]
 >gi|11094383|gb|AAG29606.1|AF217235_9 Orf9 [Staphylococcus aureus]
 >gi|11094382|gb|AAG29605.1|AF217235_8 Orf8 [Staphylococcus aureus]
 >gi|11094381|gb|AAG29604.1|AF217235_7 Orf7 [Staphylococcus aureus]
 >gi|11094380|gb|AAG29603.1|AF217235_6 Orf6 [Staphylococcus aureus]
 >gi|11094379|gb|AAG29602.1|AF217235_5 Orf5 [Staphylococcus aureus]
 >gi|11094378|gb|AAG29601.1|AF217235_4 toxic shock syndrome toxin-1 [Staphylococcus aureus]
 >gi|11094377|gb|AAG29600.1|AF217235_3 Orf3 [Staphylococcus aureus]
 >gi|11094376|gb|AAG29599.1|AF217235_2 staphylococcal enterotoxin C-bovine [Staphylococcus aureus]
 >gi|11094375|gb|AAG29598.1|AF217235_1 sel [Staphylococcus aureus]
 >gi|9944978|gb|AAG03058.1|AF288215_5 response regulator [Staphylococcus aureus]
 >gi|9944977|gb|AAG03057.1|AF288215_4 receptor histidine kinase [Staphylococcus aureus]
 >gi|9944976|gb|AAG03056.1|AF288215_3 Agr autoinducing peptide precursor [Staphylococcus aureus]
 >gi|9944975|gb|AAG03055.1|AF288215_2 putative AIP processing-secretion protein [Staphylococcus aureus]
 >gi|9944974|gb|AAG03054.1|AF288215_1 delta hemolysin [Staphylococcus aureus]
 >gi|10956173|ref|NP_048342.1| ORF64 [Staphylococcus aureus]
 >gi|10956172|ref|NP_048341.1| replication protein [Staphylococcus aureus]
 >gi|10956170|ref|NP_048340.1| ORF64 [Staphylococcus aureus]
 >gi|10956169|ref|NP_048339.1| replication protein [Staphylococcus aureus]
 >gi|10956167|ref|NP_052696.1| pot. orfB (aa 1-92) (4557 is 2nd base in codon) [Staphylococcus aureus]
 >gi|10956166|ref|NP_052695.1| pot. orfA [Staphylococcus aureus]
 >gi|10956165|ref|NP_052694.1| CAT gene (aa 1-215) [Staphylococcus aureus]
 >gi|10956164|ref|NP_052693.1| repD (aa 1-311) [Staphylococcus aureus]
 >gi|10956163|ref|NP_052692.1| unidentified reading frame [Staphylococcus aureus]
 >gi|10956161|ref|NP_052691.1| kanamycin nucleotidyltransferase (AA 1-253) [Staphylococcus aureus]
 >gi|10956160|ref|NP_052690.1| repB polypeptide (AA 1-235) [Staphylococcus aureus]
 >gi|10956158|ref|NP_052168.1| recombination protein [Staphylococcus aureus]
 >gi|10956157|ref|NP_052167.1| CAT protein [Staphylococcus aureus]
 >gi|10956156|ref|NP_052166.1| replication protein [Staphylococcus aureus]
 >gi|10956154|ref|NP_053794.1| replication protein [Staphylococcus aureus]
 >gi|10956153|ref|NP_053796.1| recombination protein [Staphylococcus aureus]
 >gi|10956152|ref|NP_053795.1| tetracycline resistance protein [Staphylococcus aureus]
 >gi|10956150|ref|NP_052130.1| beta-lactamase [Staphylococcus aureus]
 >gi|10956148|ref|NP_052129.1| beta-lactamase [Staphylococcus aureus]
 >gi|10956146|ref|NP_044360.1| tetracycline resistance protein [Staphylococcus aureus]
 >gi|10956145|ref|NP_044359.1| replication protein [Staphylococcus aureus]
 >gi|10956143|ref|NP_040438.1| reading frame D [Staphylococcus aureus]
 >gi|10956142|ref|NP_040437.1| CAT (chloramphenicol resistance) [Staphylococcus aureus]
 >gi|10956141|ref|NP_040435.1| reading frame A [Staphylococcus aureus]
 >gi|10956140|ref|NP_040436.1| reading frame C (replication) [Staphylococcus aureus]
 >gi|10946545|gb|AAG23889.1| TcaB [Staphylococcus aureus]
 >gi|10946544|gb|AAG23888.1| TcaA [Staphylococcus aureus]
 >gi|10946543|gb|AAG23887.1| TcaR [Staphylococcus aureus]
 >gi|2792490|gb|AAB97073.1| coenzyme A disulfide reductase [Staphylococcus aureus]
 >gi|10835501|pdb|1D2P|A Chain A, Crystal Structure Of Two B Repeat Units (B1b2) Of The Collagen Binding Protein (Cna) Of Staphylococcus Aureus
 >gi|10835500|pdb|1D2O|B Chain B, Crystal Structure Of A Single B Repeat Unit (B1) Of Collagen Binding Surface Protein (Cna) Of Staphylococcus Aureus.
 >gi|10835499|pdb|1D2O|A Chain A, Crystal Structure Of A Single B Repeat Unit (B1) Of Collagen Binding Surface Protein (Cna) Of Staphylococcus Aureus.
 >gi|1169372|sp|P45555|DNAJ_STAAU CHAPERONE PROTEIN DNAJ (HSP40)
 >gi|7672995|gb|AAF66692.1|AF144682_1 immunodominant antigen B [Staphylococcus aureus]
 >gi|7672993|gb|AAF66691.1|AF144681_1 immunodominant antigen A [Staphylococcus aureus]
 >gi|9955268|pdb|1QE0|B Chain B, Crystal Structure Of Apo S. Aureus Histidyl-Trna Synthetase
 >gi|9955267|pdb|1QE0|A Chain A, Crystal Structure Of Apo S. Aureus Histidyl-Trna Synthetase

>gi|9955226|pdb|1F77|B Chain B, Staphylococcal Enterotoxin H Determined To 2.4 A Resolution
 >gi|9955225|pdb|1F77|A Chain A, Staphylococcal Enterotoxin H Determined To 2.4 A Resolution
 >gi|9954962|pdb|1C79|B Chain B, Staphylokinase (Sak) Dimer
 >gi|9954961|pdb|1C79|A Chain A, Staphylokinase (Sak) Dimer
 >gi|9954960|pdb|1C78|B Chain B, Staphylokinase (Sak) Dimer
 >gi|9954959|pdb|1C78|A Chain A, Staphylokinase (Sak) Dimer
 >gi|9954958|pdb|1C77|B Chain B, Staphylokinase (Sak) Dimer
 >gi|9954957|pdb|1C77|A Chain A, Staphylokinase (Sak) Dimer
 >gi|9954956|pdb|1C76|A Chain A, Staphylokinase (Sak) Monomer
 >gi|9954208|gb|AAG08983.1|AF186237_1 ABC protein VgaA variant [Staphylococcus aureus]
 >gi|9937366|gb|AAG02426.1|AF290087_3 phosphomevalonate kinase [Staphylococcus aureus]
 >gi|9937365|gb|AAG02425.1|AF290087_2 mevalonate diphosphate decarboxylase [Staphylococcus aureus]
 >gi|9937364|gb|AAG02424.1|AF290087_1 mevalonate kinase [Staphylococcus aureus]
 >gi|9937362|gb|AAG02423.1|AF290086_2 HMG-CoA reductase [Staphylococcus aureus]
 >gi|9937361|gb|AAG02422.1|AF290086_1 HMG-CoA synthase [Staphylococcus aureus]
 >gi|7415524|dbj|BAA93438.1| FmtB [Staphylococcus aureus]
 >gi|7415419|dbj|BAA93431.1| ORF1 [Staphylococcus aureus]
 >gi|7415418|dbj|BAA93430.1| FmtB [Staphylococcus aureus]
 >gi|10121057|pdb|1FFY|A Chain A, Insights Into Editing From An Ile-Trna Synthetase Structure With Trna(Ile) And Mupirocin
 >gi|10041543|emb|CAC07605.1| unnamed protein product [Staphylococcus aureus]
 >gi|1346939|sp|P23215|QACA STAAU ANTISEPTIC RESISTANCE PROTEIN
 >gi|119116|sp|P14319|QACC STAAU QUATERNARY AMMONIUM COMPOUND-RESISTANCE PROTEIN QACC (QUATERNARY AMMONIUM DETERMINANT C) (ETHIDIUM BROMIDE RESISTANCE PROTEIN) (MULTIDRUG RESISTANCE PROTEIN)
 >gi|9971595|dbj|BAB12579.1| coagulase [Staphylococcus aureus]
 >gi|9971593|dbj|BAB12578.1| coagulase [Staphylococcus aureus]
 >gi|9971591|dbj|BAB12577.1| coagulase [Staphylococcus aureus]
 >gi|9965494|gb|AAG02249.1| peptide deformylase Pdf1 [Staphylococcus aureus]
 >gi|9931634|gb|AAG02239.1|AF295601_1 serine protease-like exoprotein E [Staphylococcus aureus]
 >gi|9931632|gb|AAG02238.1|AF295600_1 serine protease-like exoprotein A [Staphylococcus aureus]
 >gi|2494147|sp|O05338|PRIM STAAU DNA PRIMASE
 >gi|2492884|sp|Q53634|MENE STAAU O-SUCCINYLBENZOIC ACID--COA LIGASE (OSB-COA SYNTHETASE) (O-SUCCINYLBENZOATE-COA SYNTHASE)
 >gi|1703465|sp|P52081|ATL STAAU BIFUNCTIONAL AUTOLYSIN PRECURSOR [INCLUDES: N-ACETYLMURAMOYL-L-ALANINE AMIDASE ; MANNOSYL-GLYCOPROTEIN ENDO-BETA-N-ACETYLGLUCOSAMIDASE]
 >gi|136130|sp|P19380|T431 STAAU TRANSPOSASE FOR INSERTION SEQUENCE-LIKE ELEMENT IS431MEC
 >gi|136126|sp|P14506|T257 STAAU TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS257 IN TRANSPOSON TN4003
 >gi|113675|sp|P24556|ALYS STAAU AUTOLYSIN (N-ACETYLMURAMOYL-L-ALANINE AMIDASE)
 >gi|9801983|gb|AAF99572.1| replication initiation protein [Staphylococcus aureus]
 >gi|9801982|gb|AAF99571.1| unknown [Staphylococcus aureus]
 >gi|9801981|gb|AAF99570.1| recombinase [Staphylococcus aureus]
 >gi|9801980|gb|AAF99569.1| MphBM [Staphylococcus aureus]
 >gi|9801979|gb|AAF99568.1| erythromycin resistance protein [Staphylococcus aureus]
 >gi|9801978|gb|AAF99567.1| transposase [Staphylococcus aureus]
 >gi|9801977|gb|AAF99566.1| unknown [Staphylococcus aureus]
 >gi|9801976|gb|AAF99565.1| unknown [Staphylococcus aureus]
 >gi|9755015|gb|AAF98155.1|AF251216_3 FhuG [Staphylococcus aureus]
 >gi|9755014|gb|AAF98154.1|AF251216_2 FhuB [Staphylococcus aureus]
 >gi|9755013|gb|AAF98153.1|AF251216_1 FhuC [Staphylococcus aureus]
 >gi|9743649|gb|AAF97986.1| unknown [Staphylococcus aureus]
 >gi|9743648|gb|AAD33530.3|AF132117_7 unknown [Staphylococcus aureus]
 >gi|9743647|gb|AAD33529.3|AF132117_6 unknown [Staphylococcus aureus]
 >gi|9743646|gb|AAD33527.2|AF132117_4 FhuA [Staphylococcus aureus]
 >gi|9743645|gb|AAD33526.3|AF132117_3 ferrichrome transport permease [Staphylococcus aureus]
 >gi|9743644|gb|AAD33524.3|AF132117_1 ferrichrome transport permease [Staphylococcus aureus]
 >gi|9739161|gb|AAF97930.1|AF271715_6 serine protease SplF [Staphylococcus aureus]
 >gi|9739160|gb|AAF97929.1|AF271715_5 serine protease SplE [Staphylococcus aureus]
 >gi|9739159|gb|AAF97928.1|AF271715_4 serine protease SplD [Staphylococcus aureus]
 >gi|9739158|gb|AAF97927.1|AF271715_3 serine protease SplC [Staphylococcus aureus]
 >gi|9739157|gb|AAF97926.1|AF271715_2 serine protease SplB [Staphylococcus aureus]
 >gi|9739156|gb|AAF97925.1|AF271715_1 serine protease SplA [Staphylococcus aureus]
 >gi|9711569|dbj|BAB07846.1| coagulase [Staphylococcus aureus]
 >gi|9711565|dbj|BAB07845.1| coagulase [Staphylococcus aureus]
 >gi|9711561|dbj|BAB07844.1| coagulase [Staphylococcus aureus]
 >gi|9711557|dbj|BAB07843.1| coagulase [Staphylococcus aureus]
 >gi|9711553|dbj|BAB07842.1| coagulase [Staphylococcus aureus]
 >gi|9711549|dbj|BAB07841.1| coagulase [Staphylococcus aureus]
 >gi|9711545|dbj|BAB07840.1| coagulase [Staphylococcus aureus]
 >gi|9711541|dbj|BAB07839.1| coagulase [Staphylococcus aureus]
 >gi|9711537|dbj|BAB07838.1| coagulase [Staphylococcus aureus]

>gi|9711533|dbj|BAB07837.1| coagulase [Staphylococcus aureus]
 >gi|9711528|dbj|BAB07836.1| coagulase [Staphylococcus aureus]
 >gi|9711524|dbj|BAB07835.1| coagulase [Staphylococcus aureus]
 >gi|9711520|dbj|BAB07834.1| coagulase [Staphylococcus aureus]
 >gi|9711516|dbj|BAB07833.1| coagulase [Staphylococcus aureus]
 >gi|9711512|dbj|BAB07832.1| coagulase [Staphylococcus aureus]
 >gi|9711508|dbj|BAB07831.1| coagulase [Staphylococcus aureus]
 >gi|9711504|dbj|BAB07830.1| coagulase [Staphylococcus aureus]
 >gi|9711500|dbj|BAB07829.1| coagulase [Staphylococcus aureus]
 >gi|9711496|dbj|BAB07828.1| coagulase [Staphylococcus aureus]
 >gi|9711492|dbj|BAB07827.1| coagulase [Staphylococcus aureus]
 >gi|9711488|dbj|BAB07826.1| coagulase [Staphylococcus aureus]
 >gi|9711484|dbj|BAB07825.1| coagulase [Staphylococcus aureus]
 >gi|9711480|dbj|BAB07824.1| coagulase [Staphylococcus aureus]
 >gi|9622622|gb|AAF89877.1| putative site-specific recombinase XerC [Staphylococcus aureus]
 >gi|9622620|gb|AAF89876.1| putative site-specific recombinase XerD [Staphylococcus aureus]
 >gi|3806109|gb|AAC69195.1| HsdM-like protein [Staphylococcus aureus]
 >gi|3806108|gb|AAC69194.1| exotoxin 4 [Staphylococcus aureus]
 >gi|3806107|gb|AAC69193.1| exotoxin 5 [Staphylococcus aureus]
 >gi|3806106|gb|AAC69192.1| exotoxin 1 [Staphylococcus aureus]
 >gi|3806105|gb|AAC69191.1| exotoxin 3 [Staphylococcus aureus]
 >gi|3806104|gb|AAC69190.1| exotoxin 2 [Staphylococcus aureus]
 >gi|6176434|gb|AAF05589.1|AF188837_1 exotoxin 1 [Staphylococcus aureus]
 >gi|6176433|gb|AAF05588.1|AF188836_1 exotoxin 1 [Staphylococcus aureus]
 >gi|6176432|gb|AAF05587.1|AF188835_1 exotoxin 1 [Staphylococcus aureus]
 >gi|9501795|dbj|BAB03342.1| Protein A [Staphylococcus aureus]
 >gi|9501794|dbj|BAB03341.1| hypothetical protein [Staphylococcus aureus]
 >gi|9501793|dbj|BAB03340.1| hypothetical protein [Staphylococcus aureus]
 >gi|9501791|dbj|BAB03339.1| ABC transporter [Staphylococcus aureus]
 >gi|9501790|dbj|BAB03338.1| ABC transporter [Staphylococcus aureus]
 >gi|9501788|dbj|BAB03337.1| ABC transporter [Staphylococcus aureus]
 >gi|9501787|dbj|BAB03336.1| ABC transporter [Staphylococcus aureus]
 >gi|9501785|dbj|BAB03335.1| hypothetical protein [Staphylococcus aureus]
 >gi|9501784|dbj|BAB03334.1| hypothetical protein [Staphylococcus aureus]
 >gi|9501783|dbj|BAB03333.1| hypothetical protein [Staphylococcus aureus]
 >gi|9501781|dbj|BAB03332.1| fructose specific permease [Staphylococcus aureus]
 >gi|9501780|dbj|BAB03331.1| fructose 1-phosphate kinase [Staphylococcus aureus]
 >gi|9501779|dbj|BAB03330.1| fru operon repressor [Staphylococcus aureus]
 >gi|9501777|dbj|BAB03329.1| hypothetical protein [Staphylococcus aureus]
 >gi|9501776|dbj|BAB03328.1| acetyl-CoA c-acetyltransferase [Staphylococcus aureus]
 >gi|9501775|dbj|BAB03327.1| long chain fatty acid CoA ligase [Staphylococcus aureus]
 >gi|9501774|dbj|BAB03326.1| Pro/Bet transporter homolog [Staphylococcus aureus]
 >gi|9501772|dbj|BAB03325.1| response regulator [Staphylococcus aureus]
 >gi|9501771|dbj|BAB03324.1| histidine kinase sensor [Staphylococcus aureus]
 >gi|9501770|dbj|BAB03323.1| hypothetical protein [Staphylococcus aureus]
 >gi|9501769|dbj|BAB03322.1| hypothetical protein [Staphylococcus aureus]
 >gi|9501768|dbj|BAB03321.1| methionin aminopeptidase [Staphylococcus aureus]
 >gi|9501767|dbj|BAB03320.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328282|emb|CAB82465.1| catabolite control protein A [Staphylococcus aureus]
 >gi|9408171|emb|CAA71131.1| ORF213 [Staphylococcus aureus]
 >gi|9408170|emb|CAA71130.1| ORF133 [Staphylococcus aureus]
 >gi|9408169|emb|CAA71129.1| aldehyde dehydrogenase [Staphylococcus aureus]
 >gi|8895763|gb|AAF81096.1|AF228662_1 putative undecaprenol kinase [Staphylococcus aureus]
 >gi|8777467|dbj|BAA97049.1| 29-kDa cell surface protein [Staphylococcus aureus]
 >gi|7328286|emb|CAB82467.1| diaminopimelate decarboxylase [Staphylococcus aureus]
 >gi|581546|emb|CAA36783.1| AgrB protein [Staphylococcus aureus]
 >gi|581545|emb|CAA36781.1| hypothetical protein [Staphylococcus aureus]
 >gi|46600|emb|CAA37901.1| putative transposase [Staphylococcus aureus]
 >gi|46599|emb|CAA37900.1| putative transposase [Staphylococcus aureus]
 >gi|46513|emb|CAA36786.1| hypothetical protein [Staphylococcus aureus]
 >gi|46512|emb|CAA36785.1| hypothetical protein [Staphylococcus aureus]
 >gi|46511|emb|CAA36784.1| AgrA protein [Staphylococcus aureus]
 >gi|46509|emb|CAA36782.1| hypothetical protein [Staphylococcus aureus]
 >gi|46507|emb|CAA36780.1| Hld protein [Staphylococcus aureus]
 >gi|46506|emb|CAA36779.1| hypothetical protein [Staphylococcus aureus]
 >gi|9256926|pdb|1D6E|C Chain C, Crystal Structure Of Hla-Dr4 Complex With Peptidomimetic And Seb
 >gi|9256923|pdb|1D5Z|C Chain C, X-Ray Crystal Structure Of Hla-Dr4 Complexed With Peptidomimetic And Seb
 >gi|9256920|pdb|1D5X|C Chain C, X-Ray Crystal Structure Of Hla-Dr4 Complexed With Dipeptide Mimetic And Seb
 >gi|9256852|pdb|1D5M|C Chain C, X-Ray Crystal Structure Of Hla-Dr4 Complexed With Peptide And Seb

>gi|8569412|pdb|1DEE|H Chain H, Crystal Structure At 2.7a Resolution Of A Complex Between A Staphylococcus Aureus Domain And A Fab Fragment Of A Human Igm Antibody
 >gi|8569411|pdb|1DEE|G Chain G, Crystal Structure At 2.7a Resolution Of A Complex Between A Staphylococcus Aureus Domain And A Fab Fragment Of A Human Igm Antibody
 >gi|9246437|gb|AAF86053.1|AF210139_1 fmtA-like protein [Staphylococcus aureus]
 >gi|9230553|gb|AAF85897.1|AF165314_2 putative protein histidine kinase ArlS [Staphylococcus aureus]
 >gi|9230552|gb|AAF85896.1|AF165314_1 putative response regulator ArlR [Staphylococcus aureus]
 >gi|9181843|gb|AAF85653.1|orfX [Staphylococcus aureus]
 >gi|9181842|gb|AAF85652.1|orf1260 [Staphylococcus aureus]
 >gi|9181841|gb|AAF85651.1|AF181950_8 transposase [Staphylococcus aureus]
 >gi|9181840|gb|AAF85650.1|AF181950_7 alpha protein [Staphylococcus aureus]
 >gi|9181839|gb|AAF85649.1|AF181950_6 beta protein [Staphylococcus aureus]
 >gi|9181838|gb|AAF85648.1|AF181950_5 bleomycin resistance protein [Staphylococcus aureus]
 >gi|9181837|gb|AAF85647.1|AF181950_4 kanamycin resistance protein [Staphylococcus aureus]
 >gi|9181836|gb|AAF85646.1|AF181950_3 transposase [Staphylococcus aureus]
 >gi|9181835|gb|AAF85645.1|AF181950_1 low affinity penicillin binding protein [Staphylococcus aureus]
 >gi|3603441|gb|AAC35853.1|type b beta-lactamase [Staphylococcus aureus]
 >gi|8928563|sp|P81177|AURE_STAAU ZINC METALLOPROTEINASE AUREOLYSIN PRECURSOR (STAPHYLOCOCCUS AUREUS NEUTRAL PROTEINASE)
 >gi|9049372|dbj|BAA99412.1|exfoliative toxin C [Staphylococcus aureus]
 >gi|2495148|sp|Q53727|PCRA_STAAU ATP-DEPENDENT DNA HELICASE PCRA
 >gi|115038|sp|P00807|BLAC_STAAU BETA-LACTAMASE PRECURSOR (PENICILLINASE)
 >gi|3724158|emb|CAA06500.1|lipoprotein [Staphylococcus aureus]
 >gi|3724157|emb|CAA06499.1|ATP binding protein [Staphylococcus aureus]
 >gi|3724156|emb|CAA06498.1|membrane protein [Staphylococcus aureus]
 >gi|3724155|emb|CAA06497.1|membrane protein [Staphylococcus aureus]
 >gi|8885990|gb|AAF80331.1|enterotoxin I [Staphylococcus aureus]
 >gi|8648965|emb|CAB94853.1|Map-ND2C protein [Staphylococcus aureus]
 >gi|8569359|pdb|1EWC|A Chain A, Crystal Structure Of Zn²⁺ Loaded Staphylococcal Enterotoxin H
 >gi|8134803|sp|Q9ZEH3|UVR_C_STAAU EXCINUCLEASE ABC SUBUNIT C
 >gi|8134747|sp|Q9Z5C3|TPIS_STAAU TRIOSEPHOSPHATE ISOMERASE (TIM)
 >gi|8134611|sp|Q9Z5C4|PGK_STAAU PHOSPHOGLYCERATE KINASE
 >gi|8134576|sp|O86491|MURE_STAAU UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE (UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE) (MESO-DIAMINOPIMELATE-ADDING ENZYME) (UDP-MURNAC-TRIPETIDE SYNTHETASE)
 >gi|7674177|sp|Q9ZAG8|RECU_STAAU RECOMBINATION PROTEIN U HOMOLOG (PENICILLIN-BINDING PROTEIN-RELATED FACTOR A HOMOLOG) (PBP RELATED FACTOR A HOMOLOG)
 >gi|7674147|sp|Q9Z5C9|NRDI_STAAU NRDI PROTEIN
 >gi|7388052|sp|O86490|RF3_STAAU PEPTIDE CHAIN RELEASE FACTOR 3 (RF-3)
 >gi|7387927|sp|Q9ZEH5|MUS2_STAAU MUTS2 PROTEIN
 >gi|7227940|sp|P95842|RSBV_STAAU ANTI-SIGMA B FACTOR ANTAGONIST
 >gi|6920067|sp|P81683|EFG_STAAU ELONGATION FACTOR G (EF-G) (85 KDA VITRONECTIN BINDING PROTEIN)
 >gi|6686369|sp|O32418|APT_STAAU ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)
 >gi|6685442|sp|P56740|FOLB_STAAU DIHYDRONEOPTERIN ALDOLASE (DHNA)
 >gi|6651452|gb|AAF22306.1|AF189239_1 repressor of toxins Rot [Staphylococcus aureus]
 >gi|6647733|sp|O32419|REL_A_STAAU GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) ((P)PPGPP SYNTHETASE)
 >gi|6647411|sp|Q9ZAH5|ALR_STAAU ALANINE RACEMASE
 >gi|6226944|sp|O07322|MRAY_STAAU PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE (UDP-MURNAC-PENTAPEPTIDE PHOSPHOTRANSFERASE)
 >gi|6226498|sp|O05337|YSI3_STAAU HYPOTHETICAL 30.4 KDA PROTEIN IN SIGMA70 OPERON (ORF30)
 >gi|6225004|sp|Q9ZAH6|ACPS_STAAU HOLO-[ACYL-CARRIER PROTEIN] SYNTHASE (HOLO-ACP SYNTHASE)
 >gi|3913884|sp|Q59801|HYSA_STAAU HYALURONATE LYASE PRECURSOR (HYALURONIDASE) (HYASE)
 >gi|3122409|sp|O33595|MURD_STAAU UDP-N-ACETYLMURAMOYLALANINE--D-GLUTAMATE LIGASE (UDP-N-ACETYLMURAMOYL-L-ALANYL-D-GLUTAMATE SYNTHETASE) (D-GLUTAMIC ACID ADDING ENZYME)
 >gi|3122408|sp|O31211|MURC_STAAU UDP-N-ACETYLMURAMATE--ALANINE LIGASE (UDP-N-ACETYLMURAMOYL-L-ALANINE SYNTHETASE)
 >gi|2500720|sp|O06446|SECA_STAAU PREPROTEIN TRANSLOCASE SECA SUBUNIT
 >gi|2499415|sp|Q59821|ODP2_STAAU DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE COMPLEX (E2)
 >gi|2498749|sp|Q53726|PCRB_STAAU PCRB PROTEIN
 >gi|2494749|sp|Q59812|GLNA_STAAU GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) (GS)
 >gi|2492949|sp|Q59803|AROC_STAAU CHORISMATE SYNTHASE (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE)
 >gi|1723227|sp|P52080|YAT3_STAAU HYPOTHETICAL 16.6 KDA PROTEIN IN ATL 5'REGION (ORF3)
 >gi|1723225|sp|P52079|YAT2_STAAU HYPOTHETICAL 18.3 KDA PROTEIN IN ATL 5'REGION (ORF2)
 >gi|1723223|sp|P52078|YAT1_STAAU HYPOTHETICAL PROTEIN IN ATL 5'REGION (ORF1)
 >gi|1709887|sp|P51183|PT1_STAAU PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I)
 >gi|1708172|sp|P50915|HEM2_STAAU DELTA-AMINOLEVULINIC ACID DEHYDRATASE (PORPHOBILINOGEN SYNTHASE) (ALAD) (ALADH)

>gi|1174521|sp|P41972|SYI_STAAU ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)
 >gi|1172890|sp|Q02350|RECA_STAAU RECA PROTEIN
 >gi|1170027|sp|P45553|GRPE_STAAU GRPE PROTEIN (HSP-70 COFACTOR) (HSP20)
 >gi|729030|sp|P39862|CAPM_STAAU CAPM PROTEIN
 >gi|729026|sp|P39858|CAPI_STAAU CAPI PROTEIN
 >gi|586026|sp|P02976|SPA1_STAAU IMMUNOGLOBULIN G BINDING PROTEIN A PRECURSOR (IGG BINDING PROTEIN A)
 >gi|584922|sp|Q08854|CH60_STAAU 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (HEAT SHOCK PROTEIN 60)
 >gi|461535|sp|Q05615|AROA_STAAU 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) (EPSPS)
 >gi|400202|sp|P31024|LSPA_STAAU LIPOPROTEIN SIGNAL PEPTIDASE (PROLIPOPROTEIN SIGNAL PEPTIDASE) (SIGNAL PEPTIDASE II) (SPASE II)
 >gi|141181|sp|P03861|YP14_STAAU HYPOTHETICAL 14.6 KDA PROTEIN (READING FRAME C) (REPLICATION)
 >gi|136616|sp|P13954|TYSY_STAAU THYMIDYLATE SYNTHASE (TS) (TSASE)
 >gi|127193|sp|P02979|ERM2_STAAU RRNA ADENINE N-6-METHYLTRANSFERASE (MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B RESISTANCE PROTEIN) (ERYTHROMYCIN RESISTANCE PROTEIN)
 >gi|125925|sp|P11100|LACD_STAAU TAGATOSE 1,6-DIPHOSPHATE ALDOLASE (TAGATOSE-BISPHOSPHATE ALDOLASE) (D-TAGATOSE-1,6-BISPHOSPHATE ALDOLASE)
 >gi|125922|sp|P11099|LACC_STAAU TAGATOSE-6-PHOSPHATE KINASE (PHOSPHOTAGATOKINASE)
 >gi|125919|sp|P26592|LACB_STAAU GALACTOSE-6-PHOSPHATE ISOMERASE LACB SUBUNIT
 >gi|123185|sp|P01506|HLD_STAAU DELTA-HEMOLYSIN PRECURSOR (DELTA-TOXIN)
 >gi|120457|sp|P14738|FNBA_STAAU FIBRONECTIN-BINDING PROTEIN PRECURSOR (FNBP)
 >gi|113525|sp|P21545|AGRB_STAAU ACCESSORY GENE REGULATOR PROTEIN B
 >gi|8101860|gb|AAF72664.1|AF259960_1 major cold shock protein CspA [Staphylococcus aureus]
 >gi|8099634|gb|AAF72185.1|AF255950_1 AgrD signal peptide precursor [Staphylococcus aureus]
 >gi|7959131|dbj|BAA95959.1| secretory protein SAI-B [Staphylococcus aureus]
 >gi|7670327|dbj|BAA95014.1| TagG homolog [Staphylococcus aureus]
 >gi|7670326|dbj|BAA95013.1| TagH homolog [Staphylococcus aureus]
 >gi|7670325|dbj|BAA95012.1| TagA homolog [Staphylococcus aureus]
 >gi|7670324|dbj|BAA95011.1| staphylokinase [Staphylococcus aureus]
 >gi|7670323|dbj|BAA95010.1| hypothetical protein [Staphylococcus aureus]
 >gi|7670322|dbj|BAA95009.1| KdpC homolog [Staphylococcus aureus]
 >gi|7670321|dbj|BAA95008.1| KdpB homolog [Staphylococcus aureus]
 >gi|7670320|dbj|BAA95007.1| KdpA homolog [Staphylococcus aureus]
 >gi|7839534|gb|AAF70313.1|AF260326_2 SrrB [Staphylococcus aureus]
 >gi|7839533|gb|AAF70312.1|AF260326_1 SrrA [Staphylococcus aureus]
 >gi|7767013|pdb|1ENF|A Chain A, Crystal Structure Of Staphylococcal Enterotoxin H Determined To 1.69 A Resolution
 >gi|3401995|pdb|2SPZ|A Chain A, Staphylococcal Protein A, Z-Domain, Nmr, 10 Structures
 >gi|1280354|gb|AAA98144.1| ORFA [Staphylococcus aureus]
 >gi|7594777|dbj|BAA82240.2| ORF CN050 [Staphylococcus aureus]
 >gi|7594776|dbj|BAA82239.2| ORF CN049 [Staphylococcus aureus]
 >gi|7594775|dbj|BAA82233.2| ORF N065 [Staphylococcus aureus]
 >gi|7594774|dbj|BAA82227.2| ORF CN041 [Staphylococcus aureus]
 >gi|7594773|dbj|BAA82226.2| ORF CN040 [Staphylococcus aureus]
 >gi|7594772|dbj|BAA82223.2| ORF N060 [Staphylococcus aureus]
 >gi|7594771|dbj|BAA82222.2| ORF CN038 [Staphylococcus aureus]
 >gi|7594770|dbj|BAA94664.1| ORF N057 [Staphylococcus aureus]
 >gi|7594769|dbj|BAA82219.2| methicillin resistance protein MecR1 [Staphylococcus aureus]
 >gi|7594768|dbj|BAA82208.2| ORF N051 [Staphylococcus aureus]
 >gi|7594767|dbj|BAA82207.2| ORF N050 [Staphylococcus aureus]
 >gi|7594766|dbj|BAA82206.2| ORF N049 [Staphylococcus aureus]
 >gi|7594765|dbj|BAA94663.1| ORF N043 [Staphylococcus aureus]
 >gi|7594764|dbj|BAA94662.1| ORF N042 [Staphylococcus aureus]
 >gi|7594763|dbj|BAA94661.1| ORF N041 [Staphylococcus aureus]
 >gi|7594762|dbj|BAA94660.1| ORF N039 [Staphylococcus aureus]
 >gi|7594761|dbj|BAA94659.1| ORF N038 [Staphylococcus aureus]
 >gi|7594760|dbj|BAA94658.1| ORF N033 [Staphylococcus aureus]
 >gi|7594759|dbj|BAA94657.1| ORF N032 [Staphylococcus aureus]
 >gi|7594758|dbj|BAA94656.1| ORF N031 [Staphylococcus aureus]
 >gi|7594757|dbj|BAA94655.1| ORF N030 [Staphylococcus aureus]
 >gi|7594756|dbj|BAA94654.1| ORF N029 [Staphylococcus aureus]
 >gi|7594755|dbj|BAA82191.2| ORF CN018 [Staphylococcus aureus]
 >gi|7594754|dbj|BAA94653.1| ORF N024 [Staphylococcus aureus]
 >gi|7594753|dbj|BAA82189.2| ORF CN017 [Staphylococcus aureus]
 >gi|7594752|dbj|BAA82178.2| ORF CN007 [Staphylococcus aureus]
 >gi|7594751|dbj|BAA94652.1| ORF N010 [Staphylococcus aureus]
 >gi|7594750|dbj|BAA94651.1| ORF N009 [Staphylococcus aureus]
 >gi|7594749|dbj|BAA94650.1| ORF N008 [Staphylococcus aureus]
 >gi|7594748|dbj|BAA94649.1| ORF N007 [Staphylococcus aureus]
 >gi|7594747|dbj|BAA82176.2| ORF CN005 [Staphylococcus aureus]

>gi|7594746|dbj|BAA94648.1| ORF N004 [Staphylococcus aureus]
 >gi|7594745|dbj|BAA94647.1| ORF CN004 [Staphylococcus aureus]
 >gi|7594744|dbj|BAA82175.2| ORF CN003 [Staphylococcus aureus]
 >gi|7594743|dbj|BAA82173.2| ORF CN002 [Staphylococcus aureus]
 >gi|7594742|dbj|BAA82171.2| ORF CN001 [Staphylococcus aureus]
 >gi|7592634|dbj|BAA94340.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592633|dbj|BAA94339.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592632|dbj|BAA94338.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592631|dbj|BAA94337.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592630|dbj|BAA94336.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592629|dbj|BAA94335.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592628|dbj|BAA94334.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592627|dbj|BAA94333.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592626|dbj|BAA94332.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592625|dbj|BAA94331.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592624|dbj|BAA94330.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592623|dbj|BAA94329.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592622|dbj|BAA94328.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592621|dbj|BAA94327.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592620|dbj|BAA94326.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592619|dbj|BAA94325.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592618|dbj|BAA86646.3| hypothetical protein [Staphylococcus aureus]
 >gi|7592617|dbj|BAA94324.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592616|dbj|BAA94323.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592615|dbj|BAA94322.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592614|dbj|BAA86640.2| hypothetical protein [Staphylococcus aureus]
 >gi|7592613|dbj|BAA94321.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592612|dbj|BAA94320.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592611|dbj|BAA94319.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592610|dbj|BAA94318.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592609|dbj|BAA94317.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592608|dbj|BAA94316.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592607|dbj|BAA94315.1| hypothetical protein [Staphylococcus aureus]
 >gi|7592606|dbj|BAA94314.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332771|dbj|BAA86653.1| open reading frame X [Staphylococcus aureus]
 >gi|6332770|dbj|BAA86652.1| transposase [Staphylococcus aureus]
 >gi|6332769|dbj|BAA86651.1| glycerophosphoryl diester phosphodiesterase homologue [Staphylococcus aureus]
 >gi|6332768|dbj|BAA86650.1| penicillin-binding protein 2' [Staphylococcus aureus]
 >gi|6332767|dbj|BAA86649.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332766|dbj|BAA86648.1| cassette chromosome recombinase A1 [Staphylococcus aureus]
 >gi|6332765|dbj|BAA86647.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332763|dbj|BAA86645.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332762|dbj|BAA86644.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332759|dbj|BAA86641.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332757|dbj|BAA86639.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332756|dbj|BAA86638.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332755|dbj|BAA86637.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332754|dbj|BAA86636.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332753|dbj|BAA86635.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332752|dbj|BAA86634.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332751|dbj|BAA86633.1| hypothetical protein [Staphylococcus aureus]
 >gi|6332750|dbj|BAA86632.1| hypothetical protein [Staphylococcus aureus]
 >gi|5360873|dbj|BAA82243.1| orfX [Staphylococcus aureus]
 >gi|5360868|dbj|BAA82238.1| transposase for insertion sequence-like element IS43mec [Staphylococcus aureus]
 >gi|5360864|dbj|BAA82234.1| plasmid recombination enzyme [Staphylococcus aureus]
 >gi|5360860|dbj|BAA82230.1| bleomycin resistance protein (BRP) [Staphylococcus aureus]
 >gi|5360859|dbj|BAA82229.1| kanamycin nucleotidyltransferase [Staphylococcus aureus]
 >gi|5360858|dbj|BAA82228.1| transposase for insertion sequence-like element IS43mec [Staphylococcus aureus]
 >gi|5360854|dbj|BAA82224.1| glycerophosphoryldiester phosphodiesterase [Staphylococcus aureus]
 >gi|5360851|dbj|BAA82221.1| ORF N059 [Staphylococcus aureus]
 >gi|5360850|dbj|BAA82220.1| penicillin binding protein 2' [Staphylococcus aureus]
 >gi|5360848|dbj|BAA82218.1| methicillin resistance protein MecI [Staphylococcus aureus]
 >gi|5360847|dbj|BAA82217.1| ORF CN035 [Staphylococcus aureus]
 >gi|5360842|dbj|BAA82212.1| ORF CN032 [Staphylococcus aureus]
 >gi|5360841|dbj|BAA82211.1| ORF N052 [Staphylococcus aureus]
 >gi|5360840|dbj|BAA82210.1| ORF CN031 [Staphylococcus aureus]
 >gi|5360839|dbj|BAA82209.1| ORF CN030 [Staphylococcus aureus]
 >gi|5360835|dbj|BAA82205.1| rRNA adenine N-6-methyltransferase [Staphylococcus aureus]

>gi|5360834|dbj|BAA82204.1| adenyltransferase(AAD9) [Staphylococcus aureus]
 >gi|5360833|dbj|BAA82203.1| transposaseC [Staphylococcus aureus]
 >gi|5360832|dbj|BAA82202.1| transposaseB [Staphylococcus aureus]
 >gi|5360831|dbj|BAA82201.1| transposaseA [Staphylococcus aureus]
 >gi|5360826|dbj|BAA82196.1| site-specific recombinase [Staphylococcus aureus]
 >gi|5360824|dbj|BAA82194.1| site-specific recombinase [Staphylococcus aureus]
 >gi|5360818|dbj|BAA82188.1| KDP operon transcriptional regulatory protein KdpE [Staphylococcus aureus]
 >gi|5360811|dbj|BAA82181.1| potassium-transporting ATPase(B chanin) [Staphylococcus aureus]
 >gi|5360804|dbj|BAA82174.1| ORF N003 [Staphylococcus aureus]
 >gi|5360802|dbj|BAA82172.1| ORF N002 [Staphylococcus aureus]
 >gi|5360800|dbj|BAA82170.1| ORF N001 [Staphylococcus aureus]
 >gi|551990|gb|AA63529.1| dihydrolipoamide dehydrogenase E2 subunit [Staphylococcus aureus]
 >gi|152996|gb|AA63531.1| dihydrolipoamide acetyltransferase E3 subunit [Staphylococcus aureus]
 >gi|152995|gb|AA63530.1| dihydrolipoamide acetyltransferase E2 subunit [Staphylococcus aureus]
 >gi|577647|dbj|BAA07714.1| gamma-hemolysin [Staphylococcus aureus]
 >gi|7548684|gb|AAF23273.2|AF101263_3 ABC transporter MreB [Staphylococcus aureus]
 >gi|6682106|gb|AAF23274.1|AF101263_4 zinc uptake regulation protein homolog Zur [Staphylococcus aureus]
 >gi|6682104|gb|AAF23272.1|AF101263_2 ABC transporter MreA [Staphylococcus aureus]
 >gi|6682103|gb|AAF23271.1|AF101263_1 probable endonuclease IV [Staphylococcus aureus]
 >gi|4325247|gb|AAD17309.1| superoxide dismutase SodA [Staphylococcus aureus]
 >gi|7532837|gb|AAF63254.1|AF203377_2 replication initiation protein [Staphylococcus aureus]
 >gi|7532836|gb|AAF63253.1|AF203377_1 replication-associated protein [Staphylococcus aureus]
 >gi|7532834|gb|AAF63252.1|AF203376_2 replication initiation protein [Staphylococcus aureus]
 >gi|7532833|gb|AAF63251.1|AF203376_1 replication-associated protein [Staphylococcus aureus]
 >gi|7328260|emb|CAA73981.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328259|emb|CAA73980.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328258|emb|CAA73979.1| protein kinase [Staphylococcus aureus]
 >gi|7328257|emb|CAA73978.1| hypothetical protein [Staphylococcus aureus]
 >gi|510692|gb|AAA19777.1| enterotoxin H [Staphylococcus aureus]
 >gi|7522176|pir|JC7119 Drp35 protein - Staphylococcus aureus
 >gi|7470968|pir|S68971 hypothetical protein - Staphylococcus aureus
 >gi|7470967|pir|JC5470 hypothetical 29.1K protein - Staphylococcus aureus
 >gi|7470966|pir|T28680 fibrinogen-binding protein homolog - Staphylococcus aureus
 >gi|7470965|pir|T28679 fibrinogen-binding protein homolog - Staphylococcus aureus
 >gi|7470964|pir|T10908 DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - Staphylococcus aureus (fragment)
 >gi|7470963|pir|S68731 bleomycin-binding protein - Staphylococcus aureus (fragment)
 >gi|7451888|pir|S68970 triacylglycerol lipase (EC 3.1.1.3) precursor - Staphylococcus aureus
 >gi|7451316|pir|JC5468 leukocidin chain lukM precursor - Staphylococcus aureus
 >gi|7451314|pir|JC5469 Panton-Valentine leukocidin LukF-PV chain precursor - Staphylococcus aureus
 >gi|7447124|pir|T10903 acetyltransferase (EC 2.3.1.-) vatB - Staphylococcus aureus
 >gi|7443657|pir|JC5607 replication initiation protein dnaA - Staphylococcus aureus
 >gi|2145582|pir|S68609 recombinase Sin - Staphylococcus aureus plasmid pSK1
 >gi|2145581|pir|S66426 plasmin-sensitive surface protein - Staphylococcus aureus (fragments)
 >gi|2126585|pir|PN0638 vgh protein - Staphylococcus aureus
 >gi|2126584|pir|JC4555 serine-type D-Ala-D-Ala carboxypeptidase (EC 3.4.16.4) - Staphylococcus aureus
 >gi|2126583|pir|JC4511 pyroglutamyl-peptidase I (EC 3.4.19.3) - Staphylococcus aureus
 >gi|2126582|pir|S59955 hypothetical protein 202 - Staphylococcus aureus
 >gi|2126581|pir|A55598 hypothetical protein 1 - Staphylococcus aureus (fragment)
 >gi|2126580|pir|A53381 hypothetical protein (femC region) - Staphylococcus aureus (fragment)
 >gi|2126579|pir|PC4078 hlgC-like protein precursor - Staphylococcus aureus
 >gi|2126575|pir|S69209 alpha-toxin precursor - Staphylococcus aureus
 >gi|2126574|pir|PQ0040 agrD protein - Staphylococcus aureus
 >gi|2126573|pir|S58480 agrC protein - Staphylococcus aureus
 >gi|2126572|pir|JC4554 ABC-type transporter homolog - Staphylococcus aureus
 >gi|2119993|pir|C40585 recF protein - Staphylococcus aureus
 >gi|1363415|pir|S58483 hypothetical protein 8 - Staphylococcus aureus (fragment)
 >gi|1363412|pir|JC4282 gamma-hemolysin II precursor - Staphylococcus aureus
 >gi|1363410|pir|S49412 fibrinogen-binding protein precursor - Staphylococcus aureus
 >gi|1363398|pir|S55767 replication initiator repU - Staphylococcus aureus plasmid pUB110 (fragment)
 >gi|1361357|pir|S57202 vitronectin-binding surface protein - Staphylococcus aureus (fragment)
 >gi|1361356|pir|B56976 transfer protein complex trsJ - Staphylococcus aureus
 >gi|1361355|pir|S56976 transfer complex protein TrsO' - Staphylococcus aureus
 >gi|1361354|pir|A36891 transfer complex protein TrsN - Staphylococcus aureus plasmid pG01
 >gi|1361353|pir|E56976 transfer complex protein TrsM - Staphylococcus aureus
 >gi|1361352|pir|D56976 transfer complex protein trsL - Staphylococcus aureus
 >gi|1361351|pir|C56976 transfer complex protein TrsK - Staphylococcus aureus
 >gi|1361349|pir|I36891 transfer complex protein TrsH - Staphylococcus aureus

>gi|1361348|pir||H36891 transfer complex protein TrsG - Staphylococcus aureus
 >gi|1361347|pir||G36891 transfer complex protein TrsF - Staphylococcus aureus
 >gi|1361346|pir||F36891 transfer complex protein TrsE - Staphylococcus aureus
 >gi|1361345|pir||E36891 transfer complex protein TrsD - Staphylococcus aureus
 >gi|1361344|pir||D36891 transfer complex protein TrsC - Staphylococcus aureus
 >gi|1361343|pir||C36891 transfer complex protein TrsB - Staphylococcus aureus
 >gi|1361342|pir||B36891 transfer complex protein TrsA - Staphylococcus aureus
 >gi|1361341|pir||S58708 neutral phosphatase - Staphylococcus aureus (ATCC 25923) (fragment)
 >gi|1361340|pir||A55856 l1m protein - Staphylococcus aureus
 >gi|1085937|pir||S42241 hypothetical protein 5 - Staphylococcus aureus plasmid pNS1
 >gi|1085933|pir||S42240 hypothetical protein 4 - Staphylococcus aureus plasmid pNS1
 >gi|1085928|pir||S42239 hypothetical protein 3 - Staphylococcus aureus plasmid pNS1
 >gi|1085919|pir||S42237 hypothetical protein 2 - Staphylococcus aureus plasmid pNS1
 >gi|1084189|pir||S54709 hypothetical protein 81 - Staphylococcus aureus
 >gi|1075673|pir||S49271 hlgA-like protein precursor - Staphylococcus aureus
 >gi|1075672|pir||S52267 DNA polymerase III - Staphylococcus aureus
 >gi|1075671|pir||B55548 crtN protein - Staphylococcus aureus
 >gi|1075670|pir||A55548 crtM protein - Staphylococcus aureus
 >gi|1075668|pir||JC2527 alkaline shock protein - Staphylococcus aureus
 >gi|628922|pir||S43693 penicillin-binding protein 2 - Staphylococcus aureus
 >gi|543692|pir||S42238 tetracycline resistance protein - Staphylococcus aureus plasmid pNS1
 >gi|541341|pir||S42926 hypothetical membrane spanning protein - Staphylococcus aureus
 >gi|541340|pir||S42925 probable transport protein - Staphylococcus aureus
 >gi|541339|pir||S39922 pcrB protein - Staphylococcus aureus
 >gi|541336|pir||S41539 fibrinogen-binding protein - Staphylococcus aureus
 >gi|541335|pir||A48620 adhesin - Staphylococcus aureus (fragment)
 >gi|538880|pir||B24362 chloramphenicol O-acetyltransferase leader peptide - Staphylococcus aureus
 plasmid PUB112
 >gi|484391|pir||JN0627 leukocidin chain F precursor - Staphylococcus aureus
 >gi|484390|pir||JN0626 leukocidin chain S precursor - Staphylococcus aureus
 >gi|484389|pir||JN0625 gamma-hemolysin chain II precursor - Staphylococcus aureus
 >gi|482713|pir||A61069 replication protein REP - Staphylococcus aureus plasmid pOX1000
 >gi|482669|pir||A60998 replication protein REP - Staphylococcus aureus plasmid pOX2000
 >gi|481955|pir||S40262 hypothetical protein C - Staphylococcus aureus
 >gi|481954|pir||S40261 hypothetical protein B - Staphylococcus aureus
 >gi|479952|pir||S35697 leukocidin chain F - Staphylococcus aureus
 >gi|478296|pir||JN0822 acetyltransferase (EC 2.3.1.-) - Staphylococcus aureus
 >gi|478043|pir||C49238 gamma-hemolysin component, HlgC - Staphylococcus aureus
 >gi|477912|pir||B49238 gamma-hemolysin gamma 2 component, HlgB - Staphylococcus aureus
 >gi|477911|pir||B49234 leucocidin R, component F - Staphylococcus aureus
 >gi|477585|pir||A49234 leucocidin R S component - Staphylococcus aureus
 >gi|421397|pir||S11782 regulatory protein blaI - Staphylococcus aureus plasmids
 >gi|421395|pir||S11780 probable transposase - Staphylococcus aureus transposon Tn552
 >gi|421394|pir||S11781 DNA-invertase - Staphylococcus aureus transposon Tn552
 >gi|421393|pir||S11779 probable ATP-binding protein - Staphylococcus aureus transposon Tn552
 >gi|421390|pir||JN0601 heat shock protein 60 - Staphylococcus aureus
 >gi|421389|pir||JN0600 heat shock protein 10 - Staphylococcus aureus
 >gi|421388|pir||S32419 gamma-hemolysin chain H gamma II - Staphylococcus aureus
 >gi|421387|pir||S34270 fibrinogen-binding protein - Staphylococcus aureus
 >gi|421386|pir||S34269 fibrinogen-binding protein - Staphylococcus aureus
 >gi|421383|pir||S34444 blaZ protein - Staphylococcus aureus plasmid pI258 (fragment)
 >gi|421379|pir||S34447 binR protein - Staphylococcus aureus plasmid pI258 (fragment)
 >gi|322083|pir||S32211 leucocidin chain S - Staphylococcus aureus
 >gi|322082|pir||S32212 leucocidin chain F - Staphylococcus aureus
 >gi|320485|pir||A60633 tetracycline resistance protein - Staphylococcus aureus (strain MRSA101)
 >gi|320484|pir||A37389 repN protein - Staphylococcus aureus plasmid pCW7
 >gi|320483|pir||C60634 probable transposase - Staphylococcus aureus insertion sequence IS257-3
 >gi|320482|pir||B60634 probable transposase - Staphylococcus aureus insertion sequence IS257-2
 >gi|320481|pir||A60634 probable transposase - Staphylococcus aureus insertion sequence IS257-1
 >gi|320480|pir||A60757 enterotoxin C-1 - Staphylococcus aureus (fragments)
 >gi|282254|pir||A41903 recombinase homolog - Staphylococcus aureus (fragment)
 >gi|282253|pir||F42721 recombination protein recA - Staphylococcus aureus (fragment)
 >gi|282251|pir||S28101 hypothetical protein 2 - Staphylococcus aureus plasmid pC223
 >gi|282250|pir||S28102 rlx protein - Staphylococcus aureus plasmid pC223
 >gi|282249|pir||S26352 hypothetical protein - Staphylococcus aureus transposon Tn4001
 >gi|282243|pir||A42404 collagen adhesin - Staphylococcus aureus
 >gi|282241|pir||E41903 recombinase Bin3 - Staphylococcus aureus (fragment)
 >gi|282237|pir||S26353 aminoglycoside resistance protein aacA-aphD - Staphylococcus aureus
 transposon Tn4001
 >gi|282236|pir||A43848 cell surface adhesin for heparan sulfate, 66K - Staphylococcus aureus
 (fragment)

>gi|282235|pir||B43848 cell surface adhesin for heparan sulfate, 60K - *Staphylococcus aureus* (fragment)
 >gi|280218|pir||A60450 hypothetical protein att155 - *Staphylococcus aureus* (fragment)
 >gi|280217|pir||A44506 lactose operon repressor lacR - *Staphylococcus aureus*
 >gi|97855|pir||JC1204 vga protein - *Staphylococcus aureus*
 >gi|97854|pir||S12706 type II site-specific deoxyribonuclease (EC 3.1.21.4) Sau96I - *Staphylococcus aureus*
 >gi|97850|pir||A41511 staphylocoagulase precursor - *Staphylococcus aureus* (strain BB)
 >gi|97847|pir||JQ0759 restriction endonuclease (EC 3.1.-.-) - *Staphylococcus aureus*
 >gi|97846|pir||S09566 repB protein - *Staphylococcus aureus* plasmid pBD64
 >gi|97844|pir||B36242 quinolone resistance protein norA8736 - *Staphylococcus aureus* plasmid pMR8736 (fragment)
 >gi|97843|pir||S12394 probable transport protein qacA - *Staphylococcus aureus* plasmid pSK1
 >gi|97838|pir||S12093 probable transposase - *Staphylococcus aureus* insertion sequence IS431mec
 >gi|97836|pir||A36242 norA209 protein - *Staphylococcus aureus* plasmid pSA209 (fragment)
 >gi|97835|pir||A37838 norA protein - *Staphylococcus aureus*
 >gi|97834|pir||S09565 neomycin resistance protein - *Staphylococcus aureus* plasmid pBD64
 >gi|97831|pir||JQ0773 penicillin-binding protein mecA, low-affinity - *Staphylococcus aureus*
 >gi|97830|pir||S19207 leucocidin R component F precursor - *Staphylococcus aureus*
 >gi|97829|pir||A30471 hypothetical protein rep - *Staphylococcus aureus* plasmid pSK89
 >gi|97828|pir||B30471 hypothetical protein cop - *Staphylococcus aureus* plasmid pSK89
 >gi|97824|pir||S20793 hypothetical protein 5 - *Staphylococcus aureus*
 >gi|97820|pir||S12393 hypothetical protein (qacA 5' region) - *Staphylococcus aureus* plasmid pSK1
 >gi|97819|pir||S14179 hypothetical protein 140 - *Staphylococcus aureus*
 >gi|97815|pir||B38158 galactose-6-phosphate isomerase 19K chain - *Staphylococcus aureus*
 >gi|97814|pir||A38158 galactose-6-phosphate isomerase (EC 5.1.3.-) 15K chain - *Staphylococcus aureus*
 >gi|97813|pir||S19702 fibronectin-binding protein B - *Staphylococcus aureus*
 >gi|97812|pir||A32192 fibronectin-binding protein - *Staphylococcus aureus*
 >gi|97804|pir||S16509 DNA-invertase - *Staphylococcus aureus* transposon Tn552
 >gi|97795|pir||S09246 coagulase precursor - *Staphylococcus aureus* (strain 8325-4)
 >gi|97793|pir||C34643 cathepsin E (EC 3.4.23.34) - *Staphylococcus aureus* (fragments)
 >gi|97788|pir||S09385 DNA-invertase homolog bin3 - *Staphylococcus aureus* transposon Tn555
 >gi|97786|pir||S15324 beta-hemolysin - *Staphylococcus aureus*
 >gi|97783|pir||B41589 40K elastin-binding protein - *Staphylococcus aureus* (fragment)
 >gi|97782|pir||A41589 25K elastin-binding protein - *Staphylococcus aureus* (fragment)
 >gi|80324|pir||A24456 kanamycin nucleotidyltransferase (EC 2.7.7.-) - *Staphylococcus aureus* plasmid pUB110
 >gi|79917|pir||S06782 tryptophan synthase (EC 4.2.1.20) - *Staphylococcus aureus* (fragment)
 >gi|79916|pir||A24545 triacylglycerol lipase (EC 3.1.1.3) - *Staphylococcus aureus*
 >gi|79915|pir||C24584 transposition regulatory protein tnpC - *Staphylococcus aureus* transposon Tn554
 >gi|79914|pir||B24584 transposition regulatory protein tnpB - *Staphylococcus aureus* transposon Tn554
 >gi|79913|pir||A24584 transposition regulatory protein tnpA - *Staphylococcus aureus* transposon Tn554
 >gi|79912|pir||S04166 transposase 2 - *Staphylococcus aureus* transposon Tn4003
 >gi|79911|pir||S04162 transposase 1 - *Staphylococcus aureus* transposon Tn4003
 >gi|79910|pir||JS0296 transposase - *Staphylococcus aureus*
 >gi|79906|pir||S06744 staphylocoagulase precursor - *Staphylococcus aureus*
 >gi|79905|pir||A25620 staphylocoagulase - *Staphylococcus aureus* (fragment)
 >gi|79903|pir||S00935 rlx protein - *Staphylococcus aureus* plasmid pS194
 >gi|79902|pir||A29827 replication protein REP - *Staphylococcus aureus* plasmids
 >gi|79901|pir||S00909 replication initiation protein - *Staphylococcus aureus* plasmid pC223
 >gi|79900|pir||A30480 repJ protein - *Staphylococcus aureus* plasmid pC223
 >gi|79899|pir||JT0372 repI protein - *Staphylococcus aureus* plasmid pUB112
 >gi|79898|pir||S00937 repE protein - *Staphylococcus aureus* plasmid pS194
 >gi|79896|pir||A29605 protein A precursor - *Staphylococcus aureus* (strain Cowan 1)
 >gi|79894|pir||S20576 probable regulatory protein mecI - *Staphylococcus aureus*
 >gi|79891|pir||B28474 phosphotransferase system enzyme II (EC 2.7.1.69), lactose-specific, factor II - *Staphylococcus aureus*
 >gi|79887|pir||JQ1147 N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) - *Staphylococcus aureus*
 >gi|79886|pir||JQ1439 multidrug resistance protein - *Staphylococcus aureus* plasmids
 >gi|79884|pir||G29504 hypothetical 20K protein (mer regulatory region) - *Staphylococcus aureus* plasmid pI258
 >gi|79883|pir||C29504 hypothetical 24K protein (mer operon) - *Staphylococcus aureus* plasmid pI258
 >gi|79882|pir||B29504 hypothetical 18K protein (mer operon) - *Staphylococcus aureus* plasmid pI258
 >gi|79881|pir||A29504 hypothetical 16K protein (mer operon) - *Staphylococcus aureus* plasmid pI258
 >gi|79880|pir||D29504 hypothetical 14K protein (mer operon) - *Staphylococcus aureus* plasmid pI258
 >gi|79879|pir||S20575 mecR1 protein - *Staphylococcus aureus*
 >gi|79877|pir||A31901 lincomycin resistance protein linA' - *Staphylococcus aureus* (strain BM4611)
 >gi|79875|pir||JQ1530 leukocidin chain F precursor - *Staphylococcus aureus*
 >gi|79874|pir||S04359 lacD protein - *Staphylococcus aureus*
 >gi|79871|pir||S00936 hypothetical protein D - *Staphylococcus aureus* plasmid pS194
 >gi|79869|pir||S15767 hypothetical protein 2 (h1b 3' region) - *Staphylococcus aureus* (fragment)

>gi|79868|pir||S15765 hypothetical protein 1 (h1b 5' region) - Staphylococcus aureus (fragment)
 >gi|79867|pir||F24584 hypothetical protein - Staphylococcus aureus transposon Tn554
 >gi|79866|pir||S04165 hypothetical protein - Staphylococcus aureus plasmid pSK1 transposon Tn4003
 >gi|79865|pir||S06784 hypothetical protein (femA 3' region) - Staphylococcus aureus
 >gi|79864|pir||B32561 cadC protein - Staphylococcus aureus plasmid pI258
 >gi|79863|pir||A41652 probable glycerophosphodiester phosphodiesterase (EC 3.1.4.46) - Staphylococcus aureus
 >gi|79862|pir||S06783 femA protein - Staphylococcus aureus
 >gi|79857|pir||JG0016 epidermal cell differentiation inhibitor precursor - Staphylococcus aureus
 >gi|79843|pir||JQ0387 agrB protein - Staphylococcus aureus
 >gi|79842|pir||A32357 accessory gene regulatory protein agrA - Staphylococcus aureus
 >gi|7437965|pir||JC6560 UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) - Staphylococcus aureus
 >gi|7434769|pir||S34442 transcription initiation factor sigma plaC - Staphylococcus aureus
 >gi|2144945|pir||QVSAA protein A precursor - Staphylococcus aureus
 >gi|2144683|pir||ENSAC1 enterotoxin C-1 precursor - Staphylococcus aureus
 >gi|2144682|pir||ENSAB6 enterotoxin B precursor - Staphylococcus aureus
 >gi|2126578|pir||S54426 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain B - Staphylococcus aureus
 >gi|2126577|pir||S54427 gyrase-like protein alpha chain - Staphylococcus aureus
 >gi|2126576|pir||S59956 DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - Staphylococcus aureus (fragment)
 >gi|2119116|pir||S59954 ribosomal protein L7/L12 - Staphylococcus aureus (fragment)
 >gi|2117996|pir||A53641 arsenate reductase (EC 1.-.-.-) - Staphylococcus aureus plasmid pI258
 >gi|2117910|pir||S59951 DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Staphylococcus aureus
 >gi|1363411|pir||S58814 cell division protein ftsZ - Staphylococcus aureus
 >gi|1361350|pir||A56976 transfer complex protein TrsI - Staphylococcus aureus
 >gi|1084187|pir||S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Staphylococcus aureus
 >gi|1075676|pir||S54793 superoxide dismutase (EC 1.15.1.1) (Fe/Mn) - Staphylococcus aureus (fragment)
 >gi|1075669|pir||S52934 alkyl hydroperoxide reductase (EC 1.6.4.-) c22 protein - Staphylococcus aureus (fragment)
 >gi|625852|pir||JP0045 ribosomal protein L30 - Staphylococcus aureus (fragment)
 >gi|541338|pir||S39923 DNA helicase pcrA - Staphylococcus aureus
 >gi|541337|pir||S40178 isoleucine--tRNA ligase (EC 6.1.1.5) - Staphylococcus aureus
 >gi|538884|pir||B46568 ermC protein - Staphylococcus aureus plasmid pT48
 >gi|538882|pir||A40585 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain B - Staphylococcus aureus
 >gi|538881|pir||B40585 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain A - Staphylococcus aureus
 >gi|538608|pir||A24362 chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Staphylococcus aureus plasmid pUB112
 >gi|482777|pir||A61152 chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Staphylococcus aureus plasmid pSCS7
 >gi|421382|pir||S11783 bla regulator protein blaR1 - Staphylococcus aureus plasmids
 >gi|322081|pir||S32014 dihydrofolate reductase (EC 1.5.1.3) - Staphylococcus aureus
 >gi|322080|pir||A44849 chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Staphylococcus aureus plasmid
 >gi|282240|pir||B41903 arsenical resistance operon repressor - Staphylococcus aureus plasmid pI258
 >gi|282239|pir||D41903 arsenate reductase (EC 1.-.-.-) - Staphylococcus aureus plasmid pI258
 >gi|282238|pir||C41903 arsenical pump membrane protein - Staphylococcus aureus
 >gi|279459|pir||YXSAT3 thymidylate synthase (EC 2.1.1.45) - Staphylococcus aureus plasmid pSK1 transposon Tn4003
 >gi|98263|pir||A36141 cop protein - Staphylococcus aureus plasmid pE194
 >gi|97849|pir||S12705 site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) Sau96I - Staphylococcus aureus
 >gi|97842|pir||S19721 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) chain E1-beta - Staphylococcus aureus (fragment)
 >gi|97837|pir||A31048 phosphotransferase system enzyme II (EC 2.7.1.69), mannitol-specific, factor III - Staphylococcus aureus (fragments)
 >gi|97833|pir||JQ0760 methyltransferase (EC 2.1.1.-) - Staphylococcus aureus
 >gi|97832|pir||S20433 lipoprotein signal peptidase (EC 3.4.23.36) - Staphylococcus aureus
 >gi|97826|pir||S20799 hypothetical protein 7 - Staphylococcus aureus
 >gi|97816|pir||S21758 glutamic acid-specific endopeptidase - Staphylococcus aureus
 >gi|97807|pir||A33953 enterotoxin D precursor - Staphylococcus aureus
 >gi|97805|pir||S11885 enterotoxin C3 - Staphylococcus aureus
 >gi|97798|pir||S19723 dihydrolipoamide dehydrogenase (EC 1.8.1.4) - Staphylococcus aureus
 >gi|97797|pir||S19722 dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) chain E2 - Staphylococcus aureus
 >gi|97787|pir||A35001 beta-lactamase (EC 3.5.2.6) PSE-4 precursor - Staphylococcus aureus

>gi|80332|pir||B29827 macrolide/lincosamide/streptogramin B resistance methylase - Staphylococcus aureus plasmid pE5
 >gi|79907|pir||S00938 str protein - Staphylococcus aureus plasmid pS194
 >gi|79904|pir||D24584 spectinomycin resistance protein spc - Staphylococcus aureus transposon Tn554
 >gi|79893|pir||A32561 probable cadmium-transporting ATPase (EC 3.6.1.-) - Staphylococcus aureus
 >gi|79888|pir||F29504 alkylmercury lyase (EC 4.99.1.2) - Staphylococcus aureus plasmid pI258
 >gi|79885|pir||E29504 mercury(II) reductase (EC 1.16.1.1) - Staphylococcus aureus plasmid pI258
 >gi|79878|pir||A25101 erythromycin resistance protein ermA - Staphylococcus aureus transposon Tn554
 >gi|79873|pir||S04358 lacC protein - Staphylococcus aureus
 >gi|79861|pir||A26050 exfoliative toxin B precursor - Staphylococcus aureus
 >gi|79856|pir||A28179 enterotoxin E precursor - Staphylococcus aureus
 >gi|79855|pir||A60114 enterotoxin C-2 precursor - Staphylococcus aureus
 >gi|79853|pir||A28664 enterotoxin A precursor - Staphylococcus aureus
 >gi|79851|pir||S04164 dihydrofolate reductase (EC 1.5.1.3) - Staphylococcus aureus plasmid pSK1 transposon Tn4003
 >gi|79844|pir||A27233 beta-galactosidase (EC 3.2.1.23) - Staphylococcus aureus
 >gi|76321|pir||QQSAC2 hypothetical protein C - Staphylococcus aureus plasmid pC221
 >gi|76320|pir||QQSAA2 rlx protein - Staphylococcus aureus plasmid pC221
 >gi|76319|pir||QQSABT hypothetical protein B-189 - Staphylococcus aureus plasmid pT181
 >gi|76318|pir||QQAEC hypothetical protein E-229 - Staphylococcus aureus plasmid pC194
 >gi|76317|pir||QQSACC hypothetical protein C-120 - Staphylococcus aureus plasmid pC194
 >gi|76316|pir||QQA7C hypothetical protein E-74 - Staphylococcus aureus plasmid pC194
 >gi|76315|pir||QQSACE hypothetical protein C-102 - Staphylococcus aureus plasmid pE194
 >gi|76314|pir||QQSABE hypothetical protein B-111 - Staphylococcus aureus plasmid pE194
 >gi|73155|pir||RQSAD2 repD protein - Staphylococcus aureus plasmid pC221
 >gi|73154|pir||RQSACT repC protein - Staphylococcus aureus plasmids
 >gi|73152|pir||LFSAP9 ermC leader peptide - Staphylococcus aureus plasmids
 >gi|72984|pir||QQA4E hypothetical protein C-403 - Staphylococcus aureus plasmid pE194
 >gi|72843|pir||QQSACT hypothetical protein C-156 - Staphylococcus aureus plasmid pT181
 >gi|72842|pir||QQSABT hypothetical protein B-295 - Staphylococcus aureus plasmid pT181
 >gi|72420|pir||WPSAHP phosphotransferase system phosphohistidine-containing protein - Staphylococcus aureus
 >gi|69625|pir||XCSAS1 toxic shock syndrome toxin-1 precursor - Staphylococcus aureus
 >gi|69556|pir||LESAD delta hemolysin - Staphylococcus aureus
 >gi|67766|pir||PNSAP beta-lactamase (EC 3.5.2.6) precursor - Staphylococcus aureus
 >gi|67543|pir||PRSAEB epidermolytic toxin B precursor - Staphylococcus aureus plasmid pRW001
 >gi|67542|pir||PRSAEA epidermolytic toxin A precursor - Staphylococcus aureus
 >gi|67541|pir||PRSASK glutamyl endopeptidase (EC 3.4.21.19) precursor - Staphylococcus aureus
 >gi|67305|pir||NCSAF micrococcal nuclease (EC 3.1.31.1) precursor - Staphylococcus aureus
 >gi|66882|pir||PKSAF kanamycin kinase (EC 2.7.1.95) - Staphylococcus aureus
 >gi|66872|pir||WQSA3L phosphotransferase system enzyme II (EC 2.7.1.69), lactose-specific, factor III - Staphylococcus aureus
 >gi|66524|pir||XXSAC2 chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Staphylococcus aureus plasmid pC221
 >gi|66523|pir||XXSACC chloramphenicol O-acetyltransferase (EC 2.3.1.28) - Staphylococcus aureus plasmids
 >gi|66452|pir||YESA9E rRNA (adenine-N6-)-methyltransferase (EC 2.1.1.48) - Staphylococcus aureus plasmids
 >gi|7381167|gb|AAF61418.1|AF135268_1 ribonuclease P protein component [Staphylococcus aureus]
 >gi|6648971|gb|AAF21314.1| site-specific recombinase [Staphylococcus aureus]
 >gi|6648970|gb|AAF21313.1|AF118839_1 iron uptake regulatory protein; Fur [Staphylococcus aureus]
 >gi|7330783|gb|AAF60251.1| Geh [Staphylococcus aureus]
 >gi|7330782|gb|AAF60250.1| IcaC [Staphylococcus aureus]
 >gi|7330780|gb|AAF60249.1| Geh [Staphylococcus aureus]
 >gi|7330779|gb|AAF60248.1| IcaC [Staphylococcus aureus]
 >gi|7330777|gb|AAF60247.1| Geh [Staphylococcus aureus]
 >gi|7330776|gb|AAF60246.1| IcaC [Staphylococcus aureus]
 >gi|7330774|gb|AAF60245.1| Geh [Staphylococcus aureus]
 >gi|7330773|gb|AAF60244.1| IcaC [Staphylococcus aureus]
 >gi|7330771|gb|AAF60243.1| Geh [Staphylococcus aureus]
 >gi|7330770|gb|AAF60242.1| IcaC [Staphylococcus aureus]
 >gi|7330768|gb|AAF60241.1| HprK [Staphylococcus aureus]
 >gi|7330767|gb|AAF60240.1| UvrA [Staphylococcus aureus]
 >gi|7330765|gb|AAF60239.1| HprK [Staphylococcus aureus]
 >gi|7330764|gb|AAF60238.1| UvrA [Staphylococcus aureus]
 >gi|7330762|gb|AAF60237.1| HprK [Staphylococcus aureus]
 >gi|7330761|gb|AAF60236.1| UvrA [Staphylococcus aureus]
 >gi|7330759|gb|AAF60235.1| HprK [Staphylococcus aureus]
 >gi|7330758|gb|AAF60234.1| UvrA [Staphylococcus aureus]
 >gi|7330756|gb|AAF60233.1| HprK [Staphylococcus aureus]
 >gi|7330755|gb|AAF60232.1| UvrA [Staphylococcus aureus]

>gi|7330753|gb|AAF60231.1| HprK [Staphylococcus aureus]
 >gi|7330752|gb|AAF60230.1| UvrA [Staphylococcus aureus]
 >gi|6671351|gb|AAF23170.1|AF210055_3 AgrC [Staphylococcus aureus]
 >gi|6671350|gb|AAF23169.1|AF210055_2 AgrD [Staphylococcus aureus]
 >gi|6671349|gb|AAF23168.1|AF210055_1 AgrB [Staphylococcus aureus]
 >gi|7328298|emb|CAB82464.1| transketolase, putative [Staphylococcus aureus]
 >gi|7328297|emb|CAB82463.1| SOS regulatory LexA protein, putative [Staphylococcus aureus]
 >gi|7328295|emb|CAB82462.1| DNA mismatch repair protein [Staphylococcus aureus]
 >gi|7328294|emb|CAB82461.1| DNA mismatch repair protein [Staphylococcus aureus]
 >gi|7328292|emb|CAB82460.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328291|emb|CAB82459.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328290|emb|CAB82458.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328289|emb|CAB82457.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328288|emb|CAB82456.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328284|emb|CAB82466.1| MutS protein [Staphylococcus aureus]
 >gi|7328280|emb|CAB82478.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328279|emb|CAB82477.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328278|emb|CAB82476.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328277|emb|CAB82475.1| D-alanine aminotransferase [Staphylococcus aureus]
 >gi|7328276|emb|CAB82474.1| putative peptidase [Staphylococcus aureus]
 >gi|7328275|emb|CAB82473.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328274|emb|CAB82472.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328272|emb|CAB82471.1| ORF314 [Staphylococcus aureus]
 >gi|7328271|emb|CAB82470.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328270|emb|CAB82469.1| hypothetical protein [Staphylococcus aureus]
 >gi|7328269|emb|CAB82468.1| hypothetical protein [Staphylococcus aureus]
 >gi|7106006|emb|CAB75986.1| ornithine carbamoyltransferase [Staphylococcus aureus]
 >gi|7272362|gb|AAA26601.2| blaZ [Staphylococcus aureus]
 >gi|152968|gb|AAA26604.1| binR [Staphylococcus aureus]
 >gi|152967|gb|AAA26603.1| blaI [Staphylococcus aureus]
 >gi|152966|gb|AAA26602.1| blaR1 [Staphylococcus aureus]
 >gi|7242216|gb|AAB32123.2| porphobilinogen synthase; PBG; HemB [Staphylococcus aureus]
 >gi|7239722|gb|AAA71951.2| putative [Staphylococcus aureus]
 >gi|7239370|gb|AAF43206.1|AF230358_3 accessory gene regulator protein D [Staphylococcus aureus]
 >gi|7239369|gb|AAF43205.1|AF230358_2 accessory gene regulator protein B [Staphylococcus aureus]
 >gi|7239368|gb|AAF43204.1|AF230358_1 delta-haemolysin precursor [Staphylococcus aureus]
 >gi|310620|gb|AAA71964.1| putative [Staphylococcus aureus]
 >gi|310619|gb|AAA71963.1| putative [Staphylococcus aureus]
 >gi|310618|gb|AAA71962.1| putative [Staphylococcus aureus]
 >gi|310617|gb|AAA71961.1| putative [Staphylococcus aureus]
 >gi|310616|gb|AAA71960.1| putative [Staphylococcus aureus]
 >gi|310615|gb|AAA71959.1| putative [Staphylococcus aureus]
 >gi|310614|gb|AAA71958.1| putative [Staphylococcus aureus]
 >gi|310613|gb|AAA71957.1| putative [Staphylococcus aureus]
 >gi|310612|gb|AAA71956.1| putative [Staphylococcus aureus]
 >gi|310611|gb|AAA71955.1| putative [Staphylococcus aureus]
 >gi|310610|gb|AAA71954.1| putative [Staphylococcus aureus]
 >gi|310609|gb|AAA71953.1| putative [Staphylococcus aureus]
 >gi|310608|gb|AAA71952.1| putative [Staphylococcus aureus]
 >gi|4126683|dbj|BAA36693.1| enterotoxin type Gv [Staphylococcus aureus]
 >gi|7162103|emb|CAB76672.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162101|emb|CAB76671.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162099|emb|CAB76670.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162097|emb|CAB76669.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162095|emb|CAB76668.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162093|emb|CAB76667.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162091|emb|CAB76666.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162089|emb|CAB76665.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162087|emb|CAB76664.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162085|emb|CAB76663.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162083|emb|CAB76662.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162081|emb|CAB76661.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162079|emb|CAB76660.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162077|emb|CAB76659.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162075|emb|CAB76658.1| phosphate acetyltransferase [Staphylococcus aureus]
 >gi|7162073|emb|CAB76657.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162071|emb|CAB76656.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162069|emb|CAB76655.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162067|emb|CAB76654.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162065|emb|CAB76653.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|7162063|emb|CAB76652.1| triosephosphate isomerase [Staphylococcus aureus]

>gi|7161911|emb|CAB76580.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
 >gi|7161909|emb|CAB76579.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
 >gi|7161907|emb|CAB76578.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
 >gi|7161905|emb|CAB76577.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
 >gi|7161903|emb|CAB76576.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
 >gi|7161901|emb|CAB76575.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
 >gi|7161899|emb|CAB76574.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
 >gi|7161897|emb|CAB76573.1| acetyl coenzyme A acetyltransferase [Staphylococcus aureus]
 >gi|7161887|emb|CAB76839.1| Catalase [Staphylococcus aureus]
 >gi|7161885|emb|CAB76840.1| Catalase [Staphylococcus aureus]
 >gi|7107452|gb|AAF36410.1|AF235026_1 pyruvate dehydrogenase beta subunit PdhB [Staphylococcus aureus]
 >gi|7106008|emb|CAB75987.1| ornithine carbamoyltransferase Otc6850 [Staphylococcus aureus]
 >gi|7106004|emb|CAB75985.1| extracellular matrix and plasma binding protein [Staphylococcus aureus]
 >gi|7106002|emb|CAB75984.1| extracellular matrix and plasma binding protein [Staphylococcus aureus]
 >gi|7019229|emb|CAB75732.1| bone sialoprotein-binding protein [Staphylococcus aureus]
 >gi|6180191|gb|AAF05840.1|AF197058_1 trans-2-enoyl-ACP reductase [Staphylococcus aureus]
 >gi|6967305|emb|CAB72943.1| hypothetical protein [Staphylococcus aureus]
 >gi|6967304|emb|CAB72942.1| hypothetical protein [Staphylococcus aureus]
 >gi|6967303|emb|CAB72941.1| hypothetical protein [Staphylococcus aureus]
 >gi|6967301|emb|CAB72940.1| hypothetical protein [Staphylococcus aureus]
 >gi|6967300|emb|CAB72939.1| hypothetical protein [Staphylococcus aureus]
 >gi|6912039|emb|CAB72261.1| penicillin-binding protein 3 [Staphylococcus aureus]
 >gi|2506027|dbj|BAA22600.1| NAG [Staphylococcus aureus]
 >gi|577649|dbj|BAA07715.1| preLUKM [Staphylococcus aureus]
 >gi|216971|dbj|BAA00630.1| glutamic acid specific protease prepropeptide [Staphylococcus aureus]
 >gi|6119707|emb|CAB59570.1| aureolysin [Staphylococcus aureus]
 >gi|6119705|emb|CAB59569.1| aureolysin [Staphylococcus aureus]
 >gi|6119703|emb|CAB59568.1| aureolysin [Staphylococcus aureus]
 >gi|6119701|emb|CAB59567.1| aureolysin [Staphylococcus aureus]
 >gi|6729657|emb|CAB67709.1| secretory protein [Staphylococcus aureus]
 >gi|6729716|pdb|1BQB|A Chain A, Aureolysin, Staphylococcus Aureus Metalloproteinase
 >gi|5107600|pdb|1KGG|A Chain A, Structure Of Beta-Lactamase Glu166gln:asn170asp Mutant
 >gi|6110605|gb|AAF03894.1|AF193842_1 DNA polymerase I [Staphylococcus aureus]
 >gi|6690335|gb|AAF24091.1|AF117259_3 ATP binding protein VgA [Staphylococcus aureus]
 >gi|6690334|gb|AAF24090.1|AF117259_2 unknown [Staphylococcus aureus]
 >gi|6690333|gb|AAF24089.1|AF117259_1 replication protein [Staphylococcus aureus]
 >gi|6690331|gb|AAF24088.1|AF117258_5 hydrolase VgB [Staphylococcus aureus]
 >gi|6690330|gb|AAF24087.1|AF117258_4 acetyltransferase Vat [Staphylococcus aureus]
 >gi|6690329|gb|AAF24086.1|AF117258_3 resolvase [Staphylococcus aureus]
 >gi|6690328|gb|AAF24085.1|AF117258_2 unknown [Staphylococcus aureus]
 >gi|6690327|gb|AAF24084.1|AF117258_1 replication protein RepE [Staphylococcus aureus]
 >gi|6689210|emb|CAB65404.1| YycJ protein [Staphylococcus aureus]
 >gi|6689209|emb|CAB65403.1| YycI protein [Staphylococcus aureus]
 >gi|6689208|emb|CAB65402.1| YycH protein [Staphylococcus aureus]
 >gi|6689207|emb|CAB65401.1| VicK protein [Staphylococcus aureus]
 >gi|6689206|emb|CAB65400.1| TycG protein [Staphylococcus aureus]
 >gi|6689205|emb|CAB65399.1| VicR protein [Staphylococcus aureus]
 >gi|6681575|dbj|BAA88759.1| cassette chromosome recombinase B [Staphylococcus aureus]
 >gi|6681574|dbj|BAA88758.1| cassette chromosome recombinase A [Staphylococcus aureus]
 >gi|6681572|dbj|BAA88757.1| cassette chromosome recombinase B [Staphylococcus aureus]
 >gi|6681571|dbj|BAA88756.1| cassette chromosome recombinase A [Staphylococcus aureus]
 >gi|6681569|dbj|BAA88755.1| cassette chromosome recombinase B [Staphylococcus aureus]
 >gi|6681568|dbj|BAA88754.1| cassette chromosome recombinase A [Staphylococcus aureus]
 >gi|6644368|gb|AAF21032.1|AF209197_1 UDP-GlcNAc 2-epimerase [Staphylococcus aureus]
 >gi|6594284|dbj|BAA88420.1| ATP-binding protein [Staphylococcus aureus]
 >gi|6594283|dbj|BAA88419.1| hydrophobic transmembrane protein [Staphylococcus aureus]
 >gi|6594281|dbj|BAA88418.1| MsrSA [Staphylococcus aureus]
 >gi|6594280|dbj|BAA88417.1| ATP-binding protein [Staphylococcus aureus]
 >gi|6594279|dbj|BAA88416.1| hydrophobic transmembrane protein [Staphylococcus aureus]
 >gi|6594277|dbj|BAA88415.1| MsrSA [Staphylococcus aureus]
 >gi|6594276|dbj|BAA88414.1| ATP-binding protein [Staphylococcus aureus]
 >gi|6594275|dbj|BAA88413.1| hydrophobic transmembrane protein [Staphylococcus aureus]
 >gi|6578925|gb|AAF18137.1|AF205033_3 glutamyl-tRNA^{Gln} amidotransferase subunit B [Staphylococcus aureus]
 >gi|6578924|gb|AAF18136.1|AF205033_2 glutamyl-tRNA^{Gln} amidotransferase subunit A [Staphylococcus aureus]
 >gi|6578923|gb|AAF18135.1|AF205033_1 glutamyl-tRNA^{Gln} amidotransferase subunit C [Staphylococcus aureus]
 >gi|4185565|gb|AAD09131.1| surface protein Pls [Staphylococcus aureus]
 >gi|6492112|gb|AAF14183.1| putative transmembrane protein [Staphylococcus aureus]

>gi|6492111|gb|AAFL14182.1|AF105976_1 FemX [Staphylococcus aureus]
 >gi|6441050|dbj|BAA86894.1| Drp35 [Staphylococcus aureus]
 >gi|6434054|emb|CAB60756.1| permease [Staphylococcus aureus]
 >gi|6434053|emb|CAB60755.1| ATP-binding protein [Staphylococcus aureus]
 >gi|6434052|emb|CAB60754.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434050|emb|CAB60753.1| anthranilate synthase component II [Staphylococcus aureus]
 >gi|6434049|emb|CAB60752.1| anthranilate phosphoribosyltransferase [Staphylococcus aureus]
 >gi|6434048|emb|CAB60751.1| indole-3-glycerol phosphate synthase [Staphylococcus aureus]
 >gi|6434047|emb|CAB60750.1| phosphoriborylanthranilate isomerase [Staphylococcus aureus]
 >gi|6434045|emb|CAB60749.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434044|emb|CAB60748.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434042|emb|CAB60747.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434041|emb|CAB60746.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434040|emb|CAB60745.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434038|emb|CAB60744.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434037|emb|CAB60743.1| thioredoxine reductase [Staphylococcus aureus]
 >gi|6434035|emb|CAB60742.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434034|emb|CAB60741.1| hypothetical protein [Staphylococcus aureus]
 >gi|6434033|emb|CAB60740.1| thioredoxine reductase [Staphylococcus aureus]
 >gi|6434031|emb|CAB60739.1| porphobilinogen synthase [Staphylococcus aureus]
 >gi|6434030|emb|CAB60738.1| GSA-1-aminotransferase [Staphylococcus aureus]
 >gi|6434029|emb|CAB60737.1| yhjN protein [Staphylococcus aureus]
 >gi|6434028|emb|CAB60736.1| DNA-3-methyladenine glycosidase [Staphylococcus aureus]
 >gi|6273682|emb|CAA73924.1| transposase [Staphylococcus aureus]
 >gi|6273681|emb|CAA73923.1| resolvase [Staphylococcus aureus]
 >gi|6273680|emb|CAA73922.1| hypothetical protein [Staphylococcus aureus]
 >gi|6273679|emb|CAA73921.1| rRNA methylase [Staphylococcus aureus]
 >gi|6273678|emb|CAA73925.1| hypothetical protein [Staphylococcus aureus]
 >gi|6166144|sp|Q53665|DPO3_STAAU DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
 >gi|3915801|sp|P50073|PARC_STAAU TOPOISOMERASE IV SUBUNIT A
 >gi|2507345|sp|P47770|RPOC_STAAU DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN)
 (RNA POLYMERASE BETA' SUBUNIT)
 >gi|135552|sp|P02983|TCR_STAAU TETRACYCLINE RESISTANCE PROTEIN
 >gi|130885|sp|P22490|PRE2_STAAU PLASMID RECOMBINATION ENZYME (MOBILIZATION PROTEIN)
 >gi|128852|sp|P00644|NUC_STAAU THERMONUCLEASE PRECURSOR (TNASE) (MICROCOCCAL NUCLEASE)
 (STAPHYLOCOCCAL NUCLEASE)
 >gi|126941|sp|P26597|MECR_STAEF METHICILLIN RESISTANCE MECR1 PROTEIN
 >gi|6137706|pdb|1QTF|A Chain A, Crystal Structure Of Exfoliative Toxin B
 >gi|4557981|pdb|1SBB|D Chain D, T-Cell Receptor Beta Chain Complexed With Superantigen Seb
 >gi|4557979|pdb|1SBB|B Chain B, T-Cell Receptor Beta Chain Complexed With Superantigen Seb
 >gi|3025223|sp|Q53719|YLY1_STAAU HYPOTHETICAL 18.6 KD PROTEIN IN LYTA 3'REGION (ORF1)
 >gi|3911052|sp|P00731|YLLB_STAAU HYPOTHETICAL 17.4 KD PROTEIN
 >gi|2500373|sp|Q53602|YBXF_STAAU PROBABLE RIBOSOMAL PROTEIN IN RPSL 5'REGION
 >gi|2226349|gb|AAB61744.1| CspC [Staphylococcus aureus]
 >gi|2226347|gb|AAB61743.1| CspB [Staphylococcus aureus]
 >gi|1723202|sp|P55177|YAG5_STAAU HYPOTHETICAL 29.8 KD PROTEIN IN AGR OPERON (ORF 5)
 >gi|1176334|sp|P41370|YIL2_STAAU HYPOTHETICAL PROTEIN IN ILES 3'REGION (ORF C)
 >gi|1176333|sp|P41369|YIL1_STAAU HYPOTHETICAL PROTEIN IN ILES 5'REGION (ORF B)
 >gi|141232|sp|P03860|YPCD_STAAU HYPOTHETICAL 8.7 KD PROTEIN (READING FRAME D)
 >gi|141195|sp|P14503|YP2C_STAAU HYPOTHETICAL 27.7 KD PROTEIN
 >gi|141194|sp|P12052|YP2B_STAAU HYPOTHETICAL 27.0 KD PROTEIN (ORFD)
 >gi|141193|sp|P03866|YP2A_STAAU HYPOTHETICAL 26.9 KD PROTEIN (HYPOTHETICAL PROTEIN C)
 >gi|141190|sp|P23217|YP23_STAAU HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN QACA 5'REGION (ORF 188)
 >gi|141183|sp|P13977|YP15_STAAU HYPOTHETICAL 15.5 KD PROTEIN
 >gi|141180|sp|P03859|YP12_STAAU HYPOTHETICAL 12.4 KD PROTEIN (READING FRAME C)
 >gi|141043|sp|P08655|YMER_STAAU HYPOTHETICAL 19.7 KD PROTEIN IN MERCURIC RESISTANCE OPERON
 >gi|140780|sp|P21224|YHLB_STAAU HYPOTHETICAL PROTEIN IN HLB 3'REGION
 >gi|1718087|sp|P26839|VATA_STAAU VIRGINIAMYCIN A ACETYLTRANSFERASE
 >gi|138137|sp|P17978|VGB_STAAU VIRGINIAMYCIN B HYDROLASE (VGB)
 >gi|136457|sp|P06886|TSST_STAAU TOXIC SHOCK SYNDROME TOXIN-1 PRECURSOR (TSST-1)
 >gi|6094457|sp|Q53770|TETM_STAAU TETRACYCLINE RESISTANCE PROTEIN TETM (TETA(M))
 >gi|6093662|sp|Q53596|PCP_STAAU PYRROLIDONE-CARBOXYLATE PEPTIDASE (5-OXOPROLYL-PEPTIDASE)
 (PYROGLUTAMYL-PEPTIDASE I) (PGP-I) (PYRASE)
 >gi|3915844|sp|Q33276|RRF_STAAU PROBABLE RIBOSOME RECYCLING FACTOR (RIBOSOME RELEASING FACTOR) (RRF)
 >gi|3915057|sp|Q32422|SYH_STAAU HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS)
 >gi|3914612|sp|Q50581|RECG_STAAU ATP-DEPENDENT DNA HELICASE RECG
 >gi|3287914|sp|P81297|STPA_STAAU STAPHOPAIN
 >gi|3122859|sp|Q08387|SECY_STAAU PREPROTEIN TRANSLOCASE SECY SUBUNIT
 >gi|3122722|sp|Q06444|RL30_STAAU 50S RIBOSOMAL PROTEIN L30
 >gi|3024594|sp|Q06442|SECE_STAAU PREPROTEIN TRANSLOCASE SECE SUBUNIT
 >gi|3024540|sp|Q06443|RL11_STAAU 50S RIBOSOMAL PROTEIN L11

>gi|3024239|sp|O08386|NUSG_STAAU TRANSCRIPTION ANTITERMINATION PROTEIN NUSG
 >gi|2501053|sp|P95689|SYS_STAAU SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)
 >gi|2501020|sp|Q53638|SYK_STAAU LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYRS)
 >gi|2500269|sp|O06445|RL15_STAAU 50S RIBOSOMAL PROTEIN L15
 >gi|1710069|sp|P29232|RECF_STAAU RECF PROTEIN
 >gi|1709892|sp|P02907|PTHP_STAAU PHOSPHOCARRIER PROTEIN HPR (HISTIDINE-CONTAINING PROTEIN)
 >gi|1709733|sp|P51065|PPCK_STAAU PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
 >gi|1709584|sp|P50072|PARE_STAAU TOPOISOMERASE IV SUBUNIT B
 >gi|1709245|sp|P50588|NDK_STAAU NUCLEOSIDE DIPHOSPHATE KINASE (NDK) (NDP KINASE)
 >gi|1351009|sp|P48940|RS7_STAAU 30S RIBOSOMAL PROTEIN S7
 >gi|1350927|sp|P48942|RS12_STAAU 30S RIBOSOMAL PROTEIN S12
 >gi|1350849|sp|P47768|RPOB_STAAU DNA-DIRECTED RNA POLYMERASE BETA CHAIN (TRANSCRIPTASE BETA CHAIN)
 (RNA POLYMERASE BETA SUBUNIT)
 >gi|1350771|sp|P48860|RL7_STAAU 50S RIBOSOMAL PROTEIN L7/L12
 >gi|1346789|sp|P03864|PRE3_STAAU PLASMID RECOMBINATION ENZYME (MOBILIZATION PROTEIN)
 >gi|1346788|sp|P03857|PRE1_STAAU PLASMID RECOMBINATION ENZYME (MOBILIZATION PROTEIN)
 >gi|1175774|sp|P54557|PRMA_STAAU PROBABLE METHYLTRANSFERASE
 >gi|1174516|sp|P41368|SYIF_STAAU ISOLEUCYL-TRNA SYNTHETASE, MUPIROCIN RESISTANT (ISOLEUCINE--TRNA
 LIGASE) (ILERS) (MUPIROCIN RESISTANCE PROTEIN)
 >gi|1172527|sp|P45723|PLC_STAAU 1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR
 (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC)
 >gi|586104|sp|P37376|TNPF_STAAU TRANSPOSASE FOR TRANSPOSON TN554 HOMOLOG
 >gi|586103|sp|P37375|TNPE_STAAU TRANSPOSASE B (TRANSPOSON TN554 HOMOLOG)
 >gi|586027|sp|P38507|SPA2_STAAU IMMUNOGLOBULIN G BINDING PROTEIN A PRECURSOR (IGG BINDING PROTEIN A)
 >gi|548620|sp|P17875|PTMA_STAAU PTS SYSTEM, MANNITOL-SPECIFIC IIA COMPONENT (EIIA-MTL) (MANNITOL-
 PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIII-MTL)
 >gi|548619|sp|PTMA_STAAU_2 [Segment 2 of 2] PTS SYSTEM, MANNITOL-SPECIFIC IIA COMPONENT (EIIA-MTL)
 (MANNITOL-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIII-MTL)
 >gi|548618|sp|PTMA_STAAU_1 [Segment 1 of 2] PTS SYSTEM, MANNITOL-SPECIFIC IIA COMPONENT (EIIA-MTL)
 (MANNITOL-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIII-MTL)
 >gi|400965|sp|P31337|RADC_STAAU DNA REPAIR PROTEIN RADC HOMOLOG (25 KD PROTEIN)
 >gi|136146|sp|P06698|TRAC_STAAU TRANSPOSASE FOR TRANSPOSON TN554
 >gi|136133|sp|P18416|TRA3_STAAU TRANSPOSASE FOR TRANSPOSON TN552 (ORF 480)
 >gi|135956|sp|P06697|TNPB_STAAU TRANSPOSASE B (TRANSPOSON TN554)
 >gi|135955|sp|P06696|TNPA_STAAU TRANSPOSASE A (TRANSPOSON TN554)
 >gi|135949|sp|P19775|TRA6_STAAU TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS256 IN TRANSPOSON
 TN4001
 >gi|135248|sp|P23736|T2S9_STAAU TYPE II RESTRICTION ENZYME SAU96I (ENDONUCLEASE SAU96I) (R.SAU96I)
 >gi|135247|sp|P16667|T2S3_STAAU TYPE II RESTRICTION ENZYME SAU3AI (ENDONUCLEASE SAU3AI) (R.SAU3AI)
 >gi|135003|sp|P04188|STSP_STAAU GLUTAMYL ENDOPEPTIDASE PRECURSOR (STAPHYLOCOCCAL SERINE PROTEINASE)
 (V8 PROTEINASE) (ENDOPROTEINASE GLU-C)
 >gi|135002|sp|P12055|STR_STAAU STREPTOMYCIN RESISTANCE PROTEIN
 >gi|134959|sp|P17855|STC2_STAAU STAPHYLOCOAGULASE PRECURSOR
 >gi|134958|sp|P07767|STC1_STAAU STAPHYLOCOAGULASE PRECURSOR
 >gi|134189|sp|P00802|SAK_STAAU STAPHYLOKINASE PRECURSOR (NEUTRAL PROTEINASE) (PROTEASE III)
 >gi|134150|sp|P04827|S3AD_STAAU STREPTOMYCIN 3''-ADENYLYLTRANSFERASE (AAD(9))
 >gi|133479|sp|P26766|RPSD_STAAU RNA POLYMERASE SIGMA FACTOR RPOD
 >gi|133112|sp|P14491|RLX3_STAAU RLX PROTEIN
 >gi|133111|sp|P03865|RLX2_STAAU RLX PROTEIN
 >gi|133109|sp|P12054|RLX1_STAAU RLX PROTEIN
 >gi|132380|sp|P08115|REP_STAAU REPLICATION INITIATION PROTEIN
 >gi|132374|sp|P03858|REPY_STAAU REPLICATION PROTEIN
 >gi|132372|sp|P03862|REPX_STAAU REP PROTEIN (REPLICATION PROTEIN) (READING FRAME A)
 >gi|132369|sp|P19529|REPN_STAAU REPLICATION INITIATION PROTEIN
 >gi|132368|sp|P14490|REPM_STAAU REPLICATION INITIATION PROTEIN
 >gi|132364|sp|P12053|REPE_STAAU REPLICATION INITIATION PROTEIN
 >gi|132362|sp|P03065|REPD_STAAU REPLICATION INITIATION PROTEIN
 >gi|132361|sp|P03064|REPC_STAAU REPLICATION INITIATION PROTEIN (PROTEIN A)
 >gi|132357|sp|P05061|REPB_STAAU REPLICATION PROTEIN
 >gi|132322|sp|P13969|REMA_STAAU REPLICATION AND MAINTENANCE PROTEIN (PLASMID REPLICATION PROTEIN)
 >gi|131518|sp|P02909|PTLA_STAAU PTS SYSTEM, LACTOSE-SPECIFIC IIA COMPONENT (EIIA-LAC) (LACTOSE-
 PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIII-LAC)
 >gi|131497|sp|P11162|PTLB_STAAU PTS SYSTEM, LACTOSE-SPECIFIC IIBC COMPONENT (EIIBC-LAC) (LACTOSE-
 PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-LAC)
 >gi|130085|sp|P09978|PHLC_STAAU PHOSPHOLIPASE C PRECURSOR (BETA-HEMOLYSIN) (BETA-TOXIN)
 (SPHINGOMYELINASE)
 >gi|129676|sp|P07944|PBP_STAAU BETA-LACTAM-INDUCIBLE PENICILLIN-BINDING PROTEIN
 >gi|129132|sp|P21223|OMP7_STAAU 70 KD OUTER MEMBRANE PROTEIN PRECURSOR
 >gi|129123|sp|P21222|NP30_STAAU 30 KD NEUTRAL PHOSPHATASE (NPTASE)
 >gi|128511|sp|P21191|NORA_STAAU QUINOLONE RESISTANCE NORA PROTEIN

>gi|127486|sp|P23737|MTS9_STAAU MODIFICATION METHYLASE SAU96I (CYTOSINE-SPECIFIC METHYLTRANSFERASE SAU96I) (M.SAU96I)
 >gi|127485|sp|P16668|MTS3_STAAU MODIFICATION METHYLASE SAU3AI (CYTOSINE-SPECIFIC METHYLTRANSFERASE SAU3AI) (M.SAU3AI)
 >gi|6016606|sp|O68285|MSCL_STAAU LARGE-CONDUCTANCE MECHANOSENSITIVE CHANNEL
 >gi|6016162|sp|O34092|GSA_STAAU GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)
 >gi|4033454|sp|P72364|LEPH_STAAU INACTIVE SIGNAL PEPTIDASE IA
 >gi|4033452|sp|P72365|LEP_STAAU SIGNAL PEPTIDASE IB (SPASE IB) (LEADER PEPTIDASE IB)
 >gi|3122102|sp|O07325|FTSA_STAAU CELL DIVISION PROTEIN FTSA
 >gi|1709003|sp|P50307|METK_STAAU S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
 >gi|1708807|sp|P52282|LGT_STAAU PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE
 >gi|1707902|sp|P31714|GHM2_STAAU GAMMA-HEMOLYSIN H-GAMMA-II SUBUNIT
 >gi|1707901|sp|GHM2_STAAU_2 [Segment 2 of 2] GAMMA-HEMOLYSIN H-GAMMA-II SUBUNIT
 >gi|1707900|sp|GHM2_STAAU_1 [Segment 1 of 2] GAMMA-HEMOLYSIN H-GAMMA-II SUBUNIT
 >gi|1346584|sp|P80544|MRSP_STAAU METHICILLIN-RESISTANT SURFACE PROTEIN
 >gi|1346583|sp|MRSP_STAAU_7 [Segment 7 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
 >gi|1346582|sp|MRSP_STAAU_6 [Segment 6 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
 >gi|1346581|sp|MRSP_STAAU_5 [Segment 5 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
 >gi|1346580|sp|MRSP_STAAU_4 [Segment 4 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
 >gi|1346579|sp|MRSP_STAAU_3 [Segment 3 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
 >gi|1346578|sp|MRSP_STAAU_2 [Segment 2 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
 >gi|1346577|sp|MRSP_STAAU_1 [Segment 1 of 7] METHICILLIN-RESISTANT SURFACE PROTEIN
 >gi|1346244|sp|P20832|GYRB_STAAU DNA GYRASE SUBUNIT B
 >gi|1346238|sp|P20831|GYRA_STAAU DNA GYRASE SUBUNIT A
 >gi|1176137|sp|P45556|HRCA_STAAU HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
 >gi|1169769|sp|P45498|FTSZ_STAAU CELL DIVISION PROTEIN FTSZ
 >gi|547868|sp|P36884|LPCA_STAAU CHLORAMPHENICOL RESISTANCE LEADER PEPTIDE
 >gi|400204|sp|P31716|LUKS_STAAU LEUKOCIDIN S SUBUNIT PRECURSOR
 >gi|400203|sp|P31715|LUKF_STAAU LEUKOCIDIN F SUBUNIT PRECURSOR (GAMMA-HEMOLYSIN, H-GAMMA-I SUBUNIT)
 >gi|127020|sp|P08656|MERT_STAAU MERCURIC TRANSPORT PROTEIN (MERCURY ION TRANSPORT PROTEIN)
 >gi|127015|sp|P22874|MERR_STAAU MERCURIC RESISTANCE OPERON REGULATORY PROTEIN
 >gi|126999|sp|P08653|MERS_STAAU ALKYL MERCURY LYASE (ORGANOMERCURIAL LYASE)
 >gi|126995|sp|P08663|MERA_STAAU MERCURIC REDUCTASE (HG(II) REDUCTASE)
 >gi|126940|sp|P26598|MECI_STAEF METHICILLIN RESISTANCE REGULATORY PROTEIN MECI
 >gi|126446|sp|P03063|LPRM_STAAU 23S RRNA METHYLASE LEADER PEPTIDE (ERYTHROMYCIN RESISTANCE LEADER PEPTIDE)
 >gi|126333|sp|P10335|LIP_STAAU LIPASE PRECURSOR (GLYCEROL ESTER HYDROLASE)
 >gi|125937|sp|P16644|LACR_STAAU LACTOSE PHOSPHOTRANSFERASE SYSTEM REPRESSOR
 >gi|125930|sp|P11175|LACG_STAAU 6-PHOSPHO-BETA-GALACTOSIDASE (BETA-D-PHOSPHOGALACTOSIDE GALACTOHYDROLASE) (PGALASE) (P-BETA-GAL) (PBG)
 >gi|125908|sp|P26594|LACA_STAAU GALACTOSE-6-PHOSPHATE ISOMERASE LACA SUBUNIT
 >gi|125464|sp|P00554|KKA3_ENTFA AMINOGLYCOSIDE 3'-PHOSPHOTRANSFERASE (KANAMYCIN KINASE, TYPE III) (NEOMYCIN-KANAMYCIN PHOSPHOTRANSFERASE, TYPE III) (APH(3')III)
 >gi|125191|sp|P05057|KANU_STAAU KANAMYCIN NUCLEOTIDYLTRANSFERASE (NEO(R))
 >gi|123184|sp|P09616|HLA_STAAU ALPHA-HEMOLYSIN PRECURSOR (ALPHA-TOXIN) (ALPHA-HL)
 >gi|6015099|sp|O69174|ENO_STAAU ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (LAMININ BINDING PROTEIN)
 >gi|6014977|sp|Q59822|DLDH_STAAU DIHYDROLIPOAMIDE DEHYDROGENASE (E3 COMPONENT OF PYRUVATE COMPLEX) (MEMBRANE-BOUND RIBOSOME PROTEIN COMPLEX 50 KD SUBUNIT)
 >gi|6014729|sp|P81684|CS40_STAAU 40 KD VITRONECTIN-BINDING CELL SURFACE PROTEIN
 >gi|3023644|sp|O05701|DHPS_STAAU DIHYDROPTEROATE SYNTHASE (DIHYDROPTEROATE PYROPHOSPHORYLASE) (DHPS)
 >gi|2829402|sp|P49994|DNAA_STAAU CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA
 >gi|1706496|sp|P50029|DP3B_STAAU DNA POLYMERASE III, BETA CHAIN
 >gi|1169381|sp|P45554|DNAK_STAAU DNAK PROTEIN (HEAT SHOCK PROTEIN 70) (HSP70)
 >gi|544199|sp|P10167|DYRB_STAAU DIHYDROFOLATE REDUCTASE TYPE I
 >gi|462026|sp|P34071|ETC2_STAAU ENTEROTOXIN TYPE C-2 PRECURSOR (SEC2)
 >gi|127195|sp|P13978|ERM4_STAAU RRNA ADENINE N-6-METHYLTRANSFERASE (MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B RESISTANCE PROTEIN) (ERYTHROMYCIN RESISTANCE PROTEIN)
 >gi|127194|sp|P13957|ERM3_STAAU RRNA ADENINE N-6-METHYLTRANSFERASE (MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B RESISTANCE PROTEIN) (ERYTHROMYCIN RESISTANCE PROTEIN)
 >gi|127191|sp|P06699|ERM1_STAAU RRNA ADENINE N-6-METHYLTRANSFERASE (MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B RESISTANCE PROTEIN) (ERYTHROMYCIN RESISTANCE PROTEIN)
 >gi|119903|sp|P14305|FEMB_STAAU POSSIBLE PROTEIN FEMB (ORF 419)
 >gi|119902|sp|P14304|FEMA_STAAU FACTOR ESSENTIAL FOR EXPRESSION OF METHICILLIN RESISTANCE
 >gi|119655|sp|P12993|ETXE_STAAU ENTEROTOXIN TYPE E PRECURSOR (SEE)
 >gi|119654|sp|P20723|ETXD_STAAU ENTEROTOXIN TYPE D PRECURSOR (SED)
 >gi|119653|sp|P01552|ETXB_STAAU ENTEROTOXIN TYPE B PRECURSOR (SEB)
 >gi|119652|sp|P13163|ETXA_STAAU ENTEROTOXIN TYPE A PRECURSOR (SEA)
 >gi|119626|sp|P23313|ETC3_STAAU ENTEROTOXIN TYPE C-3 PRECURSOR (SEC3)

>gi|119625|sp|P01553|ETC1_STAAU ENTEROTOXIN TYPE C-1 PRECURSOR (SEC1)
 >gi|119624|sp|P09332|ETB_STAAU EXFOLIATIVE TOXIN B PRECURSOR (EPIDERMOLYTIC TOXIN B)
 >gi|119621|sp|P09331|ETA_STAAU EXFOLIATIVE TOXIN A PRECURSOR (EPIDERMOLYTIC TOXIN A)
 >gi|119131|sp|P24121|EDIN_STAAU EPIDERMAL CELL DIFFERENTIATION INHIBITOR PRECURSOR (EDIN)
 >gi|118976|sp|P13955|DYRA_STAAU DIHYDROFOLATE REDUCTASE TYPE I (TN4003)
 >gi|5813905|gb|AAD52059.1|AF086783_7 glycerol esther hydrolase [Staphylococcus aureus]
 >gi|5813904|gb|AAD52058.1|AF086783_6 IcaC [Staphylococcus aureus]
 >gi|5813903|gb|AAD52057.1|AF086783_5 IcaB [Staphylococcus aureus]
 >gi|5813902|gb|AAD52056.1|AF086783_4 IcaD [Staphylococcus aureus]
 >gi|5813901|gb|AAD52055.1|AF086783_3 IcaA [Staphylococcus aureus]
 >gi|5813900|gb|AAD52054.1|AF086783_2 IcaR [Staphylococcus aureus]
 >gi|5813899|gb|AAD52053.1|AF086783_1 CapA [Staphylococcus aureus]
 >gi|6002652|gb|AAF00080.1|AF095597_1 ferric uptake regulator homolog [Staphylococcus aureus]
 >gi|6002650|gb|AAF00079.1|AF095596_1 ferric uptake regulator homolog [Staphylococcus aureus]
 >gi|6002648|gb|AAF00078.1|AF095595_1 ferric uptake regulator homolog [Staphylococcus aureus]
 >gi|3913259|sp|Q53654|CNA_STAAU COLLAGEN ADHESIN PRECURSOR
 >gi|584919|sp|Q08841|CH10_STAAU 10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK PROTEIN 10)
 >gi|116920|sp|P25921|COP6_STAAU COP-6 PROTEIN
 >gi|1168660|sp|P20384|BIN3_STAAU POTENTIAL DNA-INVERTASE BIN3 (TRANSPOSON TN552)
 >gi|729029|sp|P39861|CAPL_STAAU CAPL PROTEIN
 >gi|729028|sp|P39860|CAPK_STAAU CAPK PROTEIN
 >gi|729027|sp|P39859|CAPJ_STAAU CAPJ PROTEIN
 >gi|729025|sp|P39857|CAPH_STAAU CAPH PROTEIN
 >gi|729024|sp|P39856|CAPG_STAAU CAPG PROTEIN
 >gi|729021|sp|P39855|CAPF_STAAU CAPF PROTEIN
 >gi|729020|sp|P39854|CAPE_STAAU CAPE PROTEIN
 >gi|729019|sp|P39853|CAPD_STAAU CAPD PROTEIN
 >gi|729018|sp|P39852|CAPC_STAAU CAPC PROTEIN
 >gi|729017|sp|P39851|CAPB_STAAU CAPB PROTEIN
 >gi|729016|sp|P39850|CAPA_STAAU CAPA PROTEIN
 >gi|584871|sp|P37374|CADF_STAAU CADMIUM EFFLUX SYSTEM ACCESSORY PROTEIN HOMOLOG
 >gi|584870|sp|P37386|CADD_STAAU PROBABLE CADMIUM-TRANSPORTING ATPASE (CADMIUM EFFLUX ATPASE)
 >gi|543935|sp|P36883|CAT5_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
 >gi|543934|sp|P36882|CAT4_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
 >gi|231569|sp|P30338|ARSR_STAAU ARSENICAL RESISTANCE OPERON REPRESSOR
 >gi|231567|sp|P30330|ARSC_STAAU ARSENATE REDUCTASE (ARSENICAL PUMP MODIFIER)
 >gi|231565|sp|P30329|ARSB_STAAU ARSENICAL PUMP MEMBRANE PROTEIN
 >gi|140340|sp|P20047|CADC_STAAU CADMIUM EFFLUX SYSTEM ACCESSORY PROTEIN
 >gi|115688|sp|P06135|CAT3_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
 >gi|115685|sp|P00486|CAT2_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
 >gi|115680|sp|P00485|CAT1_STAAU CHLORAMPHENICOL ACETYLTRANSFERASE
 >gi|115414|sp|P20021|CADA_STAAU PROBABLE CADMIUM-TRANSPORTING ATPASE (CADMIUM EFFLUX ATPASE)
 >gi|115052|sp|P22491|BLE2_STAAU BLEOMYCIN RESISTANCE PROTEIN
 >gi|115051|sp|P13014|BLE1_BACSP BLEOMYCIN RESISTANCE PROTEIN (BRP)
 >gi|115049|sp|P18357|BLAR_STAAU REGULATORY PROTEIN BLAR1
 >gi|115044|sp|P18415|BLAI_STAAU PENICILLINASE REPRESSOR (REGULATORY PROTEIN BLAI) (BETA-LACTAMASE REPRESSOR PROTEIN)
 >gi|114996|sp|P19241|BINR_STAAU DNA-INVERTASE BINR (TRANSPOSON TN552)
 >gi|114995|sp|P18358|BINL_STAAU TRANSPOSON TN552 RESOLVASE
 >gi|114300|sp|P18179|ATBP_STAAU POTENTIAL ATP-BINDING PROTEIN (ORF 271)
 >gi|3913011|sp|O05204|AHPF_STAAU ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F
 >gi|113527|sp|P13131|AGRA_STAAU ACCESSORY GENE REGULATOR PROTEIN A
 >gi|112954|sp|P14507|AACA_STAAU BIFUNCTIONAL AAC/APH [INCLUDES: 6'-AMINOGLYCOSIDE N-ACETYLTRANSFERASE (AAC(6')); 2''-AMINOGLYCOSIDE PHOSPHOTRANSFERASE (APH(2''))]
 >gi|1729798|emb|CAA71069.1| CTORF239 [Staphylococcus aureus]
 >gi|1729797|emb|CAA71068.1| sigma-B [Staphylococcus aureus]
 >gi|1729796|emb|CAA71067.1| rsbW [Staphylococcus aureus]
 >gi|1729795|emb|CAA71066.1| rsbV [Staphylococcus aureus]
 >gi|1729794|emb|CAA71065.1| rsbU [Staphylococcus aureus]
 >gi|1729793|emb|CAA71064.1| ORF136 [Staphylococcus aureus]
 >gi|1729792|emb|CAA71063.1| ORF56 [Staphylococcus aureus]
 >gi|5834651|emb|CAB55331.1| putative mannitol-specific IIA component [Staphylococcus aureus]
 >gi|5834650|emb|CAB55330.1| putative mannitol-1-phosphate 5-dehydrogenase [Staphylococcus aureus]
 >gi|5834649|emb|CAB55329.1| Mrp protein [Staphylococcus aureus]
 >gi|5834648|emb|CAA71060.2| phosphoglucosamine mutase, GlmM [Staphylococcus aureus]
 >gi|5834647|emb|CAB55328.1| hypothetical protein [Staphylococcus aureus]
 >gi|5834646|emb|CAB55327.1| hypothetical protein [Staphylococcus aureus]
 >gi|5834645|emb|CAB55326.1| arginase [Staphylococcus aureus]
 >gi|4775551|emb|CAA71062.1| CTORF1365 [Staphylococcus aureus]
 >gi|4775543|emb|CAA70781.1| arginase [Staphylococcus aureus]

>gi|4775542|emb|CAA70780.1| ORF94 [Staphylococcus aureus]
 >gi|46695|emb|CAA25094.1| protein A [Staphylococcus aureus]
 >gi|5822514|pdb|3LKF|A Chain A, Leukocidin F (Hlgb) From Staphylococcus Aureus With Phosphocholine Bound
 >gi|5822485|pdb|2LKF|A Chain A, Leukocidin F (Hlgb) From Staphylococcus Aureus
 >gi|5822083|pdb|1LKF|A Chain A, Leukocidin F (Hlgb) From Staphylococcus Aureus
 >gi|5822030|pdb|1CQV|A Chain A, Crystal Structure Of Staphylococcal Enterotoxin C2 At 100k
 >gi|5739084|gb|AAD50329.1|AF077865_1 beta-lactamase [Staphylococcus aureus]
 >gi|5726436|gb|AAD48437.1|AF162687_1 sortase [Staphylococcus aureus]
 >gi|5726302|gb|AAD48404.1|AF129010_3 CsbB homolog [Staphylococcus aureus]
 >gi|5726301|gb|AAD48403.1|AF129010_2 histidine protein kinase SaeS [Staphylococcus aureus]
 >gi|5726300|gb|AAD48402.1|AF129010_1 response regulator SaeR [Staphylococcus aureus]
 >gi|5690277|dbj|BAA13014.1|AF147744_4 transporter [Staphylococcus aureus]
 >gi|5690276|gb|AAD47013.1|AF147744_3 lantibiotic modifying enzyme [Staphylococcus aureus]
 >gi|5690275|gb|AAD47012.1|AF147744_2 lantibiotic structural protein beta [Staphylococcus aureus]
 >gi|5690274|gb|AAD47011.1|AF147744_1 lantibiotic structural protein alpha [Staphylococcus aureus]
 >gi|5672689|dbj|BAA13059.2| D-alanine-D-alanyl carrier protein ligase [Staphylococcus aureus]
 >gi|1405338|dbj|BAA13062.1| extramembranal protein [Staphylococcus aureus]
 >gi|1405337|dbj|BAA13061.1| D-alanyl carrier protein [Staphylococcus aureus]
 >gi|1405336|dbj|BAA13060.1| hypothethcal membrane transporter [Staphylococcus aureus]
 >gi|1405334|dbj|BAA13058.1| unknown [Staphylococcus aureus]
 >gi|5679714|emb|CAB51807.1| cell surface protein map-w [Staphylococcus aureus]
 >gi|5531420|emb|CAB50920.1| map-7 protein [Staphylococcus aureus]
 >gi|4558750|gb|AAD22731.1| heat shock protein 60 kDa [Staphylococcus aureus]
 >gi|4558748|gb|AAD22730.1| heat shock protein 60 kDa [Staphylococcus aureus]
 >gi|4558746|gb|AAD22729.1| heat shock protein 60 kDa [Staphylococcus aureus]
 >gi|4558744|gb|AAD22728.1| heat shock protein 60 kDa [Staphylococcus aureus]
 >gi|4558742|gb|AAD22727.1| heat shock protein 60 kDa [Staphylococcus aureus]
 >gi|4558740|gb|AAD22726.1| heat shock protein 60 kDa [Staphylococcus aureus]
 >gi|4558738|gb|AAD22725.1| heat shock protein 60 kDa [Staphylococcus aureus]
 >gi|4558736|gb|AAD22724.1| heat shock protein 60 kDa [Staphylococcus aureus]
 >gi|4558706|gb|AAD22709.1| heat shock protein 60 [Staphylococcus aureus subsp. aureus]
 >gi|4558704|gb|AAD22708.1| heat shock protein 60 [Staphylococcus aureus subsp. anaerobius]
 >gi|4205743|gb|AAD11256.1| heat shock protein 60 [Staphylococcus aureus]
 >gi|5542332|pdb|1PVL| Structure Of The Pantone-Valentine Leucocidin F Component From Staphylococcus Aureus
 >gi|2642659|gb|AAB87090.1| UDP-N-acetylmuramoyl-L-alanine synthetase [Staphylococcus aureus]
 >gi|1916729|gb|AAB51227.1| CadD [Staphylococcus aureus]
 >gi|5441303|gb|AAD43176.1|AF098801_1 penicillin-binding protein Pbp2b [Staphylococcus aureus]
 >gi|581566|emb|CAA45142.1| mecR1 [Staphylococcus aureus]
 >gi|46615|emb|CAA45143.1| mecI [Staphylococcus aureus]
 >gi|46613|emb|CAA45141.1| mecA [Staphylococcus aureus]
 >gi|5391440|dbj|BAA82253.1| orf2 [Staphylococcus aureus]
 >gi|5391439|dbj|BAA82252.1| orfX [Staphylococcus aureus]
 >gi|5391438|dbj|BAA82251.1| orf3 [Staphylococcus aureus]
 >gi|5391437|dbj|BAA82250.1| orf1 [Staphylococcus aureus]
 >gi|5327232|emb|CAB46341.1| adenine methylase [Staphylococcus aureus]
 >gi|5327231|emb|CAB46340.1| adenine methaylase [Staphylococcus aureus]
 >gi|5327230|emb|CAB46339.1| hypothetical protein [Staphylococcus aureus]
 >gi|5114231|gb|AAD40238.1|AF136709_2 histidine kinase YycG [Staphylococcus aureus]
 >gi|5114230|gb|AAD40237.1|AF136709_1 response regulator YycF [Staphylococcus aureus]
 >gi|3767595|dbj|BAA33858.1| ORF4 [Staphylococcus aureus]
 >gi|3767594|dbj|BAA33857.1| Eprh [Staphylococcus aureus]
 >gi|3767593|dbj|BAA33856.1| LytN [Staphylococcus aureus]
 >gi|3767592|dbj|BAA33855.1| ORF1 [Staphylococcus aureus]
 >gi|2605638|gb|AAB84174.1| staphylokinase [Staphylococcus aureus]
 >gi|5031413|gb|AAD38159.1|AF151117_1 replication protein [Staphylococcus aureus]
 >gi|4930180|pdb|2DHN| Complex Of 7,8-Dihydroneopterin Aldolase From Staphylococcus Aureus With 6-Hydroxymethyl-7,8-Dihydropterin At 2.2 A Resolution
 >gi|4930033|pdb|1DHN| 1.65 Angstrom Resolution Structure Of 7,8-Dihydroneopterin Aldolase From Staphylococcus Aureus
 >gi|4929299|gb|AAD33940.1|AF144661_1 factor essential for methicillin resistance [Staphylococcus aureus subsp. anaerobius]
 >gi|3892895|emb|CAA75651.1| phosphoglucosamine-mutase [Staphylococcus aureus]
 >gi|3892894|emb|CAA75650.1| hypothetical protein [Staphylococcus aureus]
 >gi|3892893|emb|CAA75649.1| hypothetical protein [Staphylococcus aureus]
 >gi|3892892|emb|CAA75648.1| arginase [Staphylococcus aureus]
 >gi|4115707|dbj|BAA36484.1| NorA [Staphylococcus aureus]
 >gi|4582216|emb|CAB40191.1| elongation factor G (EF-G) [Staphylococcus aureus]
 >gi|4574238|gb|AAD23963.1|AF106851_2 FmhC [Staphylococcus aureus]
 >gi|4574237|gb|AAD23962.1|AF106851_1 LytN [Staphylococcus aureus]

>gi|4574235|gb|AAD23961.1|AF106850_1 FmhB [Staphylococcus aureus]
 >gi|4574233|gb|AAD23960.1|AF106849_1 FmhA [Staphylococcus aureus]
 >gi|4572581|gb|AAD15142.2| Unknown [Staphylococcus aureus]
 >gi|3891901|pdb|LCV8| Staphopain, Cysteine Proteinase From Staphylococcus Aureus V8
 >gi|2981905|pdb|3NUC| Staphylococcal Nuclease, 1-N-Propane Thiol Disulfide To V23c Variant
 >gi|2981899|pdb|2NUC| Staphylococcal Nuclease, Ethane Thiol Disulfide To V23c Variant
 >gi|1942332|pdb|LSNQ| Protein Stability In Staphylococcal Nuclease
 >gi|1942331|pdb|LSNP| Protein Stability In Staphylococcal Nuclease
 >gi|1942330|pdb|LSNO| Protein Stability In Staphylococcal Nuclease
 >gi|4139848|pdb|LSSN| Staphylokinase, Sakstar Variant, Nmr, 20 Structures
 >gi|4139648|pdb|LTS5|B Chain B, I140t Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
 >gi|4139647|pdb|LTS5|A Chain A, I140t Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
 >gi|4139646|pdb|LTS4|B Chain B, Q139k Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
 >gi|4139645|pdb|LTS4|A Chain A, Q139k Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
 >gi|4139644|pdb|LTS3|C Chain C, H135a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
 >gi|4139643|pdb|LTS3|B Chain B, H135a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
 >gi|4139642|pdb|LTS3|A Chain A, H135a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
 >gi|4139641|pdb|LTS2|C Chain C, T128a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
 >gi|4139640|pdb|LTS2|B Chain B, T128a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
 >gi|4139639|pdb|LTS2|A Chain A, T128a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
 >gi|3891592|pdb|LAW7|D Chain D, Q136a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
 >gi|3891591|pdb|LAW7|C Chain C, Q136a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
 >gi|3891590|pdb|LAW7|B Chain B, Q136a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
 >gi|3891589|pdb|LAW7|A Chain A, Q136a Mutant Of Toxic Shock Syndrome Toxin-1 From S. Aureus
 >gi|4454324|emb|CAA10802.1| MapN protein [Staphylococcus aureus]
 >gi|3970797|emb|CAA74099.1| polynucleotide phosphorylase [Staphylococcus aureus]
 >gi|4530244|gb|AAD21960.1| putative exoprotein DltD [Staphylococcus aureus]
 >gi|4530243|gb|AAD21959.1| D-alanine carrier protein DltC [Staphylococcus aureus]
 >gi|4530242|gb|AAD21958.1| putative membrane protein DltB [Staphylococcus aureus]
 >gi|4530241|gb|AAD21957.1| D-alanine-D-alanyl carrier protein ligase DltA [Staphylococcus aureus]
 >gi|4530240|gb|AAD21956.1| unknown [Staphylococcus aureus]
 >gi|4490615|emb|CAB38647.1| triosephosphate isomerase [Staphylococcus aureus]
 >gi|4490614|emb|CAB38646.1| phosphoglycerate kinase [Staphylococcus aureus]
 >gi|4490613|emb|CAB38645.1| glyceraldehyde-3-phosphate dehydrogenase [Staphylococcus aureus]
 >gi|4490612|emb|CAB38644.1| gap regulator [Staphylococcus aureus]
 >gi|4490610|emb|CAB38643.1| ribonucleotide reductase minor subunit [Staphylococcus aureus]
 >gi|4490609|emb|CAB38642.1| ribonucleotide reductase major subunit [Staphylococcus aureus]
 >gi|4490608|emb|CAB38641.1| NRD1 [Staphylococcus aureus]
 >gi|4454322|emb|CAA10788.1| hypothetical protein [Staphylococcus aureus]
 >gi|4454321|emb|CAA10787.1| hypothetical protein [Staphylococcus aureus]
 >gi|4126675|dbj|BAA36689.1| Hypothetical protein [Staphylococcus aureus]
 >gi|4126674|dbj|BAA36688.1| Hypothetical protein [Staphylococcus aureus]
 >gi|4126673|dbj|BAA36687.1| CzcA [Staphylococcus aureus]
 >gi|4126672|dbj|BAA36686.1| czcD [Staphylococcus aureus]
 >gi|4126671|dbj|BAA36685.1| Hypothetical protein [Staphylococcus aureus]
 >gi|4001731|dbj|BAA35101.1| MnhG [Staphylococcus aureus]
 >gi|4001730|dbj|BAA35100.1| MnhF [Staphylococcus aureus]
 >gi|4001729|dbj|BAA35099.1| MnhE [Staphylococcus aureus]
 >gi|4001728|dbj|BAA35098.1| MnhD [Staphylococcus aureus]
 >gi|4001727|dbj|BAA35097.1| MnhC [Staphylococcus aureus]
 >gi|4001726|dbj|BAA35096.1| MnhB [Staphylococcus aureus]
 >gi|4001725|dbj|BAA35095.1| MnhA [Staphylococcus aureus]
 >gi|4001724|dbj|BAA35094.1| OrfA [Staphylococcus aureus]
 >gi|3694944|gb|AAC62498.1| SirC [Staphylococcus aureus]
 >gi|3694943|gb|AAC62497.1| SirB [Staphylococcus aureus]
 >gi|3694942|gb|AAC62496.1| lipoprotein SirA [Staphylococcus aureus]
 >gi|4138456|emb|CAA11555.1| Map protein [Staphylococcus aureus]
 >gi|4138445|emb|CAA77018.1| adenine methylase [Staphylococcus aureus]
 >gi|3955031|emb|CAA76853.1| PBP2 [Staphylococcus aureus]
 >gi|3955030|emb|CAA76852.1| unknown [Staphylococcus aureus]
 >gi|3550596|emb|CAA06652.1| sdr E [Staphylococcus aureus]
 >gi|3550594|emb|CAA06651.1| sdrD [Staphylococcus aureus]
 >gi|3550592|emb|CAA06650.1| sdrC [Staphylococcus aureus]
 >gi|809080|emb|CAA24595.1| reading frame [Staphylococcus aureus]
 >gi|3320606|gb|AAD09875.1| putative heme A synthase [Staphylococcus aureus]
 >gi|4104230|gb|AAD01977.1| phospho-N-acetylmuramoyl-pentapeptide translocase [Staphylococcus aureus]
 >gi|4103900|gb|AAD01884.1| 60 kDa heat shock protein [Staphylococcus aureus]
 >gi|4097757|gb|AAD00167.1| lytic regulatory protein [Staphylococcus aureus]
 >gi|4090655|gb|AAC98834.1| ORF64 [Staphylococcus aureus]
 >gi|4090654|gb|AAC98833.1| replication protein [Staphylococcus aureus]
 >gi|4090652|gb|AAC98832.1| ORF64 [Staphylococcus aureus]

>gi|4090651|gb|AAC98831.1| replication protein [Staphylococcus aureus]
 >gi|2811118|gb|AAC95492.1| unknown [Staphylococcus aureus]
 >gi|2811115|gb|AAC95491.1| unknown [Staphylococcus aureus]
 >gi|4009497|gb|AAC95464.1| cell division protein DivIVA [Staphylococcus aureus]
 >gi|4009496|gb|AAC95463.1| YlmH [Staphylococcus aureus]
 >gi|4009495|gb|AAC95462.1| YlmG [Staphylococcus aureus]
 >gi|4009494|gb|AAC95461.1| YlmF [Staphylococcus aureus]
 >gi|4009493|gb|AAC95460.1| YlmE [Staphylococcus aureus]
 >gi|4009492|gb|AAC95459.1| YlmD [Staphylococcus aureus]
 >gi|4009491|gb|AAC95458.1| cell division protein FtsZ [Staphylococcus aureus]
 >gi|1402771|gb|AAC80254.1| major cold-shock protein [Staphylococcus aureus]
 >gi|3372542|gb|AAC78590.1| enterotoxin J [Staphylococcus aureus]
 >gi|3372541|gb|AAC78589.1| enterotoxin D [Staphylococcus aureus]
 >gi|3892644|dbj|BAA34540.1| MphBM [Staphylococcus aureus]
 >gi|3892643|dbj|BAA34539.1| MsrSA [Staphylococcus aureus]
 >gi|3892642|dbj|BAA34538.1| leader peptide [Staphylococcus aureus]
 >gi|3850852|emb|CAA76222.1| hypothetical protein [Staphylococcus aureus]
 >gi|3850851|emb|CAA76221.1| alr protein [Staphylococcus aureus]
 >gi|3850850|emb|CAA76220.1| dpj protein [Staphylococcus aureus]
 >gi|3850849|emb|CAA76219.1| hypothetical protein [Staphylococcus aureus]
 >gi|3850848|emb|CAA76218.1| hypothetical protein [Staphylococcus aureus]
 >gi|3850847|emb|CAA76217.1| hypothetical protein [Staphylococcus aureus]
 >gi|3850846|emb|CAA76216.1| kpdC protein [Staphylococcus aureus]
 >gi|3800828|gb|AAC69846.1| oligopeptide transporter putative ATPase domain [Staphylococcus aureus]
 >gi|3800827|gb|AAC69845.1| oligopeptide transporter putative ATPase domain [Staphylococcus aureus]
 >gi|3800826|gb|AAC69844.1| oligopeptide transporter putative membrane permease domain [Staphylococcus aureus]
 >gi|3800825|gb|AAC69843.1| oligopeptide transporter putative membrane permease domain [Staphylococcus aureus]
 >gi|3800823|gb|AAC69842.1| unknown [Staphylococcus aureus]
 >gi|3800822|gb|AAC69841.1| oligopeptide transporter putative ATPase domain [Staphylococcus aureus]
 >gi|3800821|gb|AAC69840.1| oligopeptide transporter putative ATPase domain [Staphylococcus aureus]
 >gi|3800820|gb|AAC69839.1| oligopeptide transporter putative membrane permease domain [Staphylococcus aureus]
 >gi|3800819|gb|AAC69838.1| oligopeptide transporter putative membrane permease domain [Staphylococcus aureus]
 >gi|3800818|gb|AAC69837.1| oligopeptide transporter putative substrate binding domain [Staphylococcus aureus]
 >gi|2765304|emb|CAA73668.1| leukotoxin, LukD [Staphylococcus aureus]
 >gi|2765303|emb|CAA73667.1| leukotoxin LukE [Staphylococcus aureus]
 >gi|3212829|pdb|5NUC| Staphylococcal Nuclease, 1-N-Pentane Thiol Disulfide To V23c Variant
 >gi|3212819|pdb|3SEB| Staphylococcal Enterotoxin B
 >gi|2982145|pdb|2SAK| Staphylokinase (Sakstar Variant)
 >gi|2914575|pdb|7AHL|G Chain G, Alpha-Hemolysin From Staphylococcus Aureus
 >gi|2914574|pdb|7AHL|F Chain F, Alpha-Hemolysin From Staphylococcus Aureus
 >gi|2914573|pdb|7AHL|E Chain E, Alpha-Hemolysin From Staphylococcus Aureus
 >gi|2914572|pdb|7AHL|D Chain D, Alpha-Hemolysin From Staphylococcus Aureus
 >gi|2914571|pdb|7AHL|C Chain C, Alpha-Hemolysin From Staphylococcus Aureus
 >gi|2914570|pdb|7AHL|B Chain B, Alpha-Hemolysin From Staphylococcus Aureus
 >gi|2914569|pdb|7AHL|A Chain A, Alpha-Hemolysin From Staphylococcus Aureus
 >gi|2914205|pdb|2SEB|D Chain D, X-Ray Crystal Structure Of Hla-Dr4 Complexed With A Peptide From Human Collagen II
 >gi|2780937|pdb|5TSS|B Chain B, Toxic Shock Syndrome Toxin-1: Orthorhombic P222(1) Crystal Form
 >gi|2780936|pdb|5TSS|A Chain A, Toxic Shock Syndrome Toxin-1: Orthorhombic P222(1) Crystal Form
 >gi|2780930|pdb|4TSS| Toxic Shock Syndrome Toxin-1: Tetragonal P4(1)2(1)2 Crystal Form
 >gi|2780925|pdb|3TSS| Toxic Shock Syndrome Toxin-1 Tetramutant, P2(1) Crystal Form
 >gi|2780919|pdb|2TSS|C Chain C, Toxic Shock Syndrome Toxin-1 From Staphylococcus Aureus: Orthorhombic P222(1) Crystal Form
 >gi|2780918|pdb|2TSS|B Chain B, Toxic Shock Syndrome Toxin-1 From Staphylococcus Aureus: Orthorhombic P222(1) Crystal Form
 >gi|2780917|pdb|2TSS|A Chain A, Toxic Shock Syndrome Toxin-1 From Staphylococcus Aureus: Orthorhombic P222(1) Crystal Form
 >gi|2392714|pdb|2QIL|C Chain C, Toxic Shock Syndrome Toxin-1 At 2.07 A Resolution
 >gi|2392713|pdb|2QIL|B Chain B, Toxic Shock Syndrome Toxin-1 At 2.07 A Resolution
 >gi|2392712|pdb|2QIL|A Chain A, Toxic Shock Syndrome Toxin-1 At 2.07 A Resolution
 >gi|1310952|pdb|2SOB| Sn-Ob, Ob-Fold Sub-Domain Of Staphylococcal Nuclease, Nmr, 10 Structures
 >gi|2781288|pdb|1SXT|B Chain B, Staphylococcal Enterotoxin Type A (Sea) Co-Crystallised With Zinc
 >gi|2781287|pdb|1SXT|A Chain A, Staphylococcal Enterotoxin Type A (Sea) Co-Crystallised With Zinc
 >gi|2624726|pdb|1SE4| Staphylococcal Enterotoxin B Complexed With Lactose
 >gi|2392546|pdb|1SE3| Staphylococcal Enterotoxin B Complexed With Gm3 Trisaccharide

>gi|2098291|pdb|1SND|B Chain B, Staphylococcal Nuclease Dimer Containing A Deletion Of Residues 114-119 Complexed With Calcium Chloride And The Competitive Inhibitor Deoxythymidine-3',5'-Diphosphate
 >gi|2098290|pdb|1SND|A Chain A, Staphylococcal Nuclease Dimer Containing A Deletion Of Residues 114-119 Complexed With Calcium Chloride And The Competitive Inhibitor Deoxythymidine-3',5'-Diphosphate
 >gi|1942753|pdb|1STE| Staphylococcal Enterotoxin C2 From Staphylococcus Aureus
 >gi|1633348|pdb|1SEB|H Chain H, Complex Of The Human Mhc Class Ii Glycoprotein Hla-Dri And The Bacterial Superantigen Seb
 >gi|1633344|pdb|1SEB|D Chain D, Complex Of The Human Mhc Class Ii Glycoprotein Hla-Dri And The Bacterial Superantigen Seb
 >gi|1431724|pdb|1SE2| Staphylococcal Enterotoxin C2, Monoclinic Form
 >gi|3212584|pdb|1OME|B Chain B, Crystal Structure Of The Omega Loop Deletion Mutant (Residues 163 - 178 Deleted) Of Beta-Lactamase From Staphylococcus Aureus Pcl
 >gi|3212583|pdb|1OME|A Chain A, Crystal Structure Of The Omega Loop Deletion Mutant (Residues 163 - 178 Deleted) Of Beta-Lactamase From Staphylococcus Aureus Pcl
 >gi|2392515|pdb|1QIL|C Chain C, Inactive Mutant Toxic Shock Syndrome Toxin-1 At 2.5 A
 >gi|2392514|pdb|1QIL|B Chain B, Inactive Mutant Toxic Shock Syndrome Toxin-1 At 2.5 A
 >gi|2392513|pdb|1QIL|A Chain A, Inactive Mutant Toxic Shock Syndrome Toxin-1 At 2.5 A
 >gi|2392479|pdb|1NUC| Staphylococcal Nuclease, V23c Variant
 >gi|2624537|pdb|1JCK|D Chain D, T-Cell Receptor Beta Chain Complexed With Sec3 Superantigen
 >gi|2624535|pdb|1JCK|B Chain B, T-Cell Receptor Beta Chain Complexed With Sec3 Superantigen
 >gi|2098496|pdb|1KGE| Structure Of Beta-Lactamase Asn 170 Met Mutant
 >gi|1942204|pdb|1KGF| Structure Of Beta-Lactamase Asn 170 Gln Mutant
 >gi|1827772|pdb|1KNY|B Chain B, Kanamycin Nucleotidyltransferase
 >gi|1827771|pdb|1KNY|A Chain A, Kanamycin Nucleotidyltransferase
 >gi|2982092|pdb|1EXF|A Chain A, Exfoliative Toxin A
 >gi|2098519|pdb|1EDI| Staphylococcal Protein A E-Domain (-60), Nmr, 22 Structures
 >gi|2098517|pdb|1EDI| Staphylococcal Protein A E-Domain (180), Nmr, Minimized Average Structure
 >gi|2098516|pdb|1EDJ| Staphylococcal Protein A E-Domain (180), Nmr, 20 Structures
 >gi|2098515|pdb|1EDK| Staphylococcal Protein A E-Domain (-60), Nmr, Minimized Average Structure
 >gi|1942144|pdb|1DJC| Structure Of Beta-Lactamase Precursor, S70a Mutant, At 120k
 >gi|1942143|pdb|1DJB| Structure Of Beta-Lactamase Precursor, S70a Mutant, At 298k
 >gi|1942142|pdb|1DJA| Structure Of Beta-Lactamase Precursor, K73h Mutant, At 298k
 >gi|1633233|pdb|1ESF|B Chain B, Staphylococcal Enterotoxin A
 >gi|1633232|pdb|1ESF|A Chain A, Staphylococcal Enterotoxin A
 >gi|1942696|pdb|1BDD| Staphylococcus Aureus Protein A, Immunoglobulin-Binding B Domain, Nmr, Minimized Average Structure
 >gi|1942695|pdb|1BDC| Staphylococcus Aureus Protein A, Immunoglobulin-Binding B Domain, Nmr, 10 Structures
 >gi|3318765|pdb|1AMX| Collagen-Binding Domain From A Staphylococcus Aureus Adhesin
 >gi|3212427|pdb|1AD4|B Chain B, Dihydropteroate Synthetase Complexed With Oh-Ch2-Pterin-Pyrophosphate From Staphylococcus Aureus
 >gi|3212426|pdb|1AD4|A Chain A, Dihydropteroate Synthetase Complexed With Oh-Ch2-Pterin-Pyrophosphate From Staphylococcus Aureus
 >gi|3212425|pdb|1AD1|B Chain B, Dihydropteroate Synthetase (Apo Form) From Staphylococcus Aureus
 >gi|3212424|pdb|1AD1|A Chain A, Dihydropteroate Synthetase (Apo Form) From Staphylococcus Aureus
 >gi|2554719|pdb|1AGJ|B Chain B, Epidermolytic Toxin A From Staphylococcus Aureus
 >gi|2554718|pdb|1AGJ|A Chain A, Epidermolytic Toxin A From Staphylococcus Aureus
 >gi|2554635|pdb|1ALQ| Circularly Permuted Beta-Lactamase From Staphylococcus Aureus Pcl
 >gi|2392077|pdb|1AEX| Staphylococcal Nuclease, Methane Thiol Disulfide To V23c Variant
 >gi|3212327|pdb|1A3V| Staphylococcal Nuclease, Cyclopentane Thiol Disulfide To V23c Variant
 >gi|3212326|pdb|1A3U| Staphylococcal Nuclease, Cyclohexane Thiol Disulfide To V23c Variant
 >gi|3212325|pdb|1A3T| Staphylococcal Nuclease, V23c Variant, Complex With 2-Fluoroethane Thiol And 3',5'-Thymidine Diphosphate
 >gi|3212274|pdb|1A2U| Staphylococcal Nuclease, V23c Variant, Complex With 1-N-Butane Thiol And 3',5'-Thymidine Diphosphate
 >gi|3212273|pdb|1A2T| Staphylococcal Nuclease, B-Mercaptoethanol Disulfide To V23c Variant
 >gi|3776113|emb|CAA11406.1| succinate dehydrogenase complex, cytochrome b558 subunit [Staphylococcus aureus]
 >gi|3776112|emb|CAA11405.1| excinuclease ABC, subunit C [Staphylococcus aureus]
 >gi|3776111|emb|CAA11404.1| thioredoxin [Staphylococcus aureus]
 >gi|3776110|emb|CAA11403.1| MutS-like protein [Staphylococcus aureus]
 >gi|3747042|gb|AAC64162.1| tyrosine recombinase XerD [Staphylococcus aureus]
 >gi|3676411|gb|AAC63227.1| putative transposase TnpE [Staphylococcus aureus]
 >gi|3676410|gb|AAC63226.1| thymidylate synthetase ThyE [Staphylococcus aureus]
 >gi|3676409|gb|AAC63225.1| trimethoprim resistance protein DfrA [Staphylococcus aureus]
 >gi|3676408|gb|AAC63224.1| unknown [Staphylococcus aureus]
 >gi|3676407|gb|AAC63223.1| putative transposase TnpD [Staphylococcus aureus]
 >gi|3676406|gb|AAC63222.1| replication protein Rep [Staphylococcus aureus]
 >gi|3676405|gb|AAC63221.1| putative transposase TnpC [Staphylococcus aureus]
 >gi|3676456|gb|AAC61974.1| putative transposase TnpG [Staphylococcus aureus]
 >gi|3676455|gb|AAC61973.1| putative transposase TnpF [Staphylococcus aureus]

>gi|3676454|gb|AAC61972.1| bifunctional aminoglycoside modifying enzyme AacA-AphD [Staphylococcus aureus]
 >gi|3676453|gb|AAC61971.1| unknown [Staphylococcus aureus]
 >gi|3676452|gb|AAC61970.1| putative transposase TnpE [Staphylococcus aureus]
 >gi|3676451|gb|AAC61969.1| multidrug resistance efflux protein Smr [Staphylococcus aureus]
 >gi|3676450|gb|AAC61968.1| putative replication initiation protein Rep(RC) [Staphylococcus aureus]
 >gi|3676449|gb|AAC61967.1| putative transposase TnpD [Staphylococcus aureus]
 >gi|3676448|gb|AAC61966.1| unknown [Staphylococcus aureus]
 >gi|3676447|gb|AAC61965.1| putative single-stranded DNA binding protein TraM [Staphylococcus aureus]
 >gi|3676446|gb|AAC61964.1| putative membrane protein TraL [Staphylococcus aureus]
 >gi|3676445|gb|AAC61963.1| putative membrane protein TraK [Staphylococcus aureus]
 >gi|3676444|gb|AAC61962.1| putative membrane protein TraJ [Staphylococcus aureus]
 >gi|3676443|gb|AAC61961.1| putative topoisomerase TraI [Staphylococcus aureus]
 >gi|3676442|gb|AAC61960.1| lipoprotein TraH [Staphylococcus aureus]
 >gi|3676441|gb|AAC61959.1| putative membrane protein TraG [Staphylococcus aureus]
 >gi|3676440|gb|AAC61958.1| putative membrane protein TraF [Staphylococcus aureus]
 >gi|3676439|gb|AAC61957.1| putative ATPase TraE [Staphylococcus aureus]
 >gi|3676438|gb|AAC61956.1| TraD [Staphylococcus aureus]
 >gi|3676437|gb|AAC61955.1| putative membrane protein TraC [Staphylococcus aureus]
 >gi|3676436|gb|AAC61954.1| putative membrane protein TraB [Staphylococcus aureus]
 >gi|3676435|gb|AAC61953.1| TraA [Staphylococcus aureus]
 >gi|3676434|gb|AAC61952.1| putative regulator of transfer genes ArtA [Staphylococcus aureus]
 >gi|3676433|gb|AAC61951.1| putative transposase TnpC [Staphylococcus aureus]
 >gi|3676432|gb|AAC61950.1| aminoglycoside adenyltransferase AadD [Staphylococcus aureus]
 >gi|3676431|gb|AAC61949.1| bleomycin resistance protein Ble [Staphylococcus aureus]
 >gi|3676430|gb|AAC61948.1| Pre [Staphylococcus aureus]
 >gi|3676429|gb|AAC61947.1| putative transposase TnpB [Staphylococcus aureus]
 >gi|3676428|gb|AAC61946.1| membrane protein [Staphylococcus aureus]
 >gi|3676427|gb|AAC61945.1| putative transposase TnpA [Staphylococcus aureus]
 >gi|3676426|gb|AAC61944.1| putative replication initiation protein Rep [Staphylococcus aureus]
 >gi|3676425|gb|AAC61943.1| unknown [Staphylococcus aureus]
 >gi|3676424|gb|AAC61942.1| unknown [Staphylococcus aureus]
 >gi|3676423|gb|AAC61941.1| unknown [Staphylococcus aureus]
 >gi|3676422|gb|AAC61940.1| putative membrane protein [Staphylococcus aureus]
 >gi|3676421|gb|AAC61939.1| unknown [Staphylococcus aureus]
 >gi|3676420|gb|AAC61938.1| oriT nickase Nes [Staphylococcus aureus]
 >gi|3676419|gb|AAC61937.1| LtrC-like protein [Staphylococcus aureus]
 >gi|3676418|gb|AAC61936.1| unknown [Staphylococcus aureus]
 >gi|3676417|gb|AAC61935.1| unknown [Staphylococcus aureus]
 >gi|3676416|gb|AAC61934.1| putative resolvase Res [Staphylococcus aureus]
 >gi|3676415|gb|AAC61933.1| unknown [Staphylococcus aureus]
 >gi|3676414|gb|AAC61932.1| unknown [Staphylococcus aureus]
 >gi|3676413|gb|AAC61931.1| unknown [Staphylococcus aureus]
 >gi|410007|gb|AAC60446.1| leukocidin F component [Staphylococcus aureus, MRSA No. 4, Peptide, 323 aa]
 >gi|410006|gb|AAC60445.1| leukocidin S component [Staphylococcus aureus, MRSA No. 4, Peptide, 315 aa]
 >gi|410005|gb|AAC60444.1| gamma-hemolysin II, H gamma II [Staphylococcus aureus, MRSA No. 4, Peptide, 309 aa]
 >gi|2271510|gb|AAC46291.1| UDP-N-acetylmuramoyl-L-alanine : D-glutamate ligase; MurD [Staphylococcus aureus]
 >gi|1773355|gb|AAC46099.1| Cap5P [Staphylococcus aureus]
 >gi|1773354|gb|AAC46098.1| Cap5O [Staphylococcus aureus]
 >gi|1773353|gb|AAC46097.1| Cap5N [Staphylococcus aureus]
 >gi|1773352|gb|AAC46096.1| Cap5M [Staphylococcus aureus]
 >gi|1773351|gb|AAC46095.1| Cap5L [Staphylococcus aureus]
 >gi|1773350|gb|AAC46094.1| Cap5K [Staphylococcus aureus]
 >gi|1773349|gb|AAC46093.1| Cap5J [Staphylococcus aureus]
 >gi|1773348|gb|AAC46092.1| Cap5I [Staphylococcus aureus]
 >gi|1773347|gb|AAC46091.1| Cap5H [Staphylococcus aureus]
 >gi|1773346|gb|AAC46090.1| Cap5G [Staphylococcus aureus]
 >gi|1773345|gb|AAC46089.1| Cap5F [Staphylococcus aureus]
 >gi|1773344|gb|AAC46088.1| Cap5E [Staphylococcus aureus]
 >gi|1773343|gb|AAC46087.1| Cap5D [Staphylococcus aureus]
 >gi|1773342|gb|AAC46086.1| Cap5C [Staphylococcus aureus]
 >gi|1773341|gb|AAC46085.1| Cap5B [Staphylococcus aureus]
 >gi|1773340|gb|AAC46084.1| Cap5A [Staphylococcus aureus]
 >gi|1673629|gb|AAC46100.1| O-acetyl transferase [Staphylococcus aureus]
 >gi|706922|gb|AAC46354.1| ribosomal protein S7 [Staphylococcus aureus]
 >gi|706921|gb|AAC46353.1| ribosomal protein S12 [Staphylococcus aureus]
 >gi|706920|gb|AAC46352.1| unknown [Staphylococcus aureus]

>gi|2589184|gb|AAC45836.1| GSA-1-aminotransferase [Staphylococcus aureus]
 >gi|2589183|gb|AAC45835.1| d-aminolevulinic acid dehydratase [Staphylococcus aureus]
 >gi|2589182|gb|AAC45834.1| uroporphyrinogen III synthase [Staphylococcus aureus]
 >gi|2589181|gb|AAC45833.1| porphobilinogen deaminase [Staphylococcus aureus]
 >gi|2149898|gb|AAC45629.1| cell division protein [Staphylococcus aureus]
 >gi|2149897|gb|AAC45628.1| cell division protein [Staphylococcus aureus]
 >gi|2149896|gb|AAC45627.1| cell division protein [Staphylococcus aureus]
 >gi|2149895|gb|AAC45626.1| D-glutamic acid adding enzyme [Staphylococcus aureus]
 >gi|2149894|gb|AAC45625.1| phospho-N-muramic acid-pentapeptide translocase [Staphylococcus aureus]
 >gi|2149893|gb|AAC45624.1| penicillin-binding protein 1 [Staphylococcus aureus]
 >gi|2149892|gb|AAC45623.1| cell division protein [Staphylococcus aureus]
 >gi|2149891|gb|AAC45622.1| unknown [Staphylococcus aureus]
 >gi|2149890|gb|AAC45621.1| unknown [Staphylococcus aureus]
 >gi|1314302|gb|AAC45357.1| isoleucyl-tRNA synthetase [Staphylococcus aureus]
 >gi|1314301|gb|AAC45356.1| unknown [Staphylococcus aureus]
 >gi|1575026|gb|AAC44840.1| LrgB
 >gi|1575025|gb|AAC44839.1| holin-like protein LrgA
 >gi|710422|gb|AAC44803.1| cmp-binding-factor 1
 >gi|710421|gb|AAC44802.1| unknown
 >gi|1595810|gb|AAC44435.1| type-I signal peptidase SpsB [Staphylococcus aureus]
 >gi|1595809|gb|AAC44434.1| type-I signal peptidase SpsA [Staphylococcus aureus]
 >gi|1397239|gb|AAC44135.1| elastin binding protein
 >gi|1001961|gb|AAC43470.1| MHC class II analog
 >gi|3327949|gb|AAC38785.1| putative recombinase Sin [Staphylococcus aureus]
 >gi|3327948|gb|AAC38784.1| multidrug efflux protein QacB [Staphylococcus aureus]
 >gi|3327947|gb|AAC38783.1| transcriptional regulator QacR [Staphylococcus aureus]
 >gi|3327945|gb|AAC38782.1| putative transposase TnpA [Staphylococcus aureus]
 >gi|3327944|gb|AAC38781.1| delta-orf186 [Staphylococcus aureus]
 >gi|3327943|gb|AAC38780.1| multidrug efflux protein QacB [Staphylococcus aureus]
 >gi|3327942|gb|AAC38779.1| transcriptional regulator QacR [Staphylococcus aureus]
 >gi|3135292|gb|AAC38560.1| large conductance mechanosensitive channel [Staphylococcus aureus]
 >gi|2827912|gb|AAC38446.1| IgG-binding protein SBI [Staphylococcus aureus]
 >gi|2565311|gb|AAC38087.1| high affinity proline permease [Staphylococcus aureus]
 >gi|2315995|gb|AAC38146.1| branched-chain amino acid carrier protein [Staphylococcus aureus]
 >gi|4379428|emb|CAA11546.1| thioredoxin reductase [Staphylococcus aureus]
 >gi|3445567|gb|AAC32485.1| transport protein [Staphylococcus aureus]
 >gi|3445566|gb|AAC32484.1| repressor protein [Staphylococcus aureus]
 >gi|3411114|gb|AAC31156.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
 >gi|3411112|gb|AAC31155.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
 >gi|3411110|gb|AAC31154.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
 >gi|3411108|gb|AAC31153.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
 >gi|3411106|gb|AAC31152.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
 >gi|3411104|gb|AAC31151.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
 >gi|3411102|gb|AAC31150.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
 >gi|3411100|gb|AAC31149.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
 >gi|3411098|gb|AAC31148.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
 >gi|3411096|gb|AAC31147.1| DNA topoisomerase IV subunit A [Staphylococcus aureus]
 >gi|3411092|gb|AAC31144.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
 >gi|3411090|gb|AAC31143.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
 >gi|3411088|gb|AAC31142.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
 >gi|3411086|gb|AAC31141.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
 >gi|3411084|gb|AAC31140.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
 >gi|3411082|gb|AAC31139.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
 >gi|3411080|gb|AAC31138.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
 >gi|3411078|gb|AAC31137.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
 >gi|3411076|gb|AAC31136.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
 >gi|3411074|gb|AAC31135.1| DNA gyrase subunit A; topoisomerase [Staphylococcus aureus]
 >gi|2689564|gb|AAC28969.1| integrase [Staphylococcus aureus]
 >gi|2689563|gb|AAC28968.1| enterotoxin [Staphylococcus aureus]
 >gi|2689562|gb|AAC28967.1| orf15 [Staphylococcus aureus]
 >gi|2689561|gb|AAC28966.1| orf14 [Staphylococcus aureus]
 >gi|2689560|gb|AAC28965.1| orf13 [Staphylococcus aureus]
 >gi|2689559|gb|AAC28964.1| orf12 [Staphylococcus aureus]
 >gi|2689558|gb|AAC28963.1| orf11 [Staphylococcus aureus]
 >gi|2689557|gb|AAC28962.1| orf10 [Staphylococcus aureus]
 >gi|2689556|gb|AAC28961.1| orf9 [Staphylococcus aureus]
 >gi|2689555|gb|AAC28960.1| orf8 [Staphylococcus aureus]
 >gi|2689554|gb|AAC28959.1| orf7 [Staphylococcus aureus]
 >gi|2689553|gb|AAC28958.1| orf6 [Staphylococcus aureus]
 >gi|2689552|gb|AAC28957.1| orf5 [Staphylococcus aureus]
 >gi|2689551|gb|AAC28956.1| orf4 [Staphylococcus aureus]

>gi|2689550|gb|AAC28955.1| orf3 [Staphylococcus aureus]
 >gi|2689549|gb|AAC28954.1| toxic shock syndrome toxin-1 [Staphylococcus aureus]
 >gi|2689548|gb|AAC28953.1| orf1 [Staphylococcus aureus]
 >gi|3393011|emb|CAA12115.1| Clumping factor B [Staphylococcus aureus]
 >gi|3323613|gb|AAC26661.1| extracellular enterotoxin type I precursor [Staphylococcus aureus]
 >gi|3323611|gb|AAC26660.1| extracellular enterotoxin type G precursor [Staphylococcus aureus]
 >gi|3256224|emb|CAA74741.1| ypfP [Staphylococcus aureus]
 >gi|3256223|emb|CAA74740.1| UDP-N-acetylmuramyl-tripeptide synthetase [Staphylococcus aureus]
 >gi|3256222|emb|CAA74739.1| peptide chain release factor 3 [Staphylococcus aureus]
 >gi|230814|pdb|3BLM| Beta-Lactamase (E.C.3.5.2.6)
 >gi|230746|pdb|2SNS| Staphylococcal Nuclease (E.C.3.1.33.1) Complex With 2(Prime)-Deoxy-3(Prime)-5(Prime)-Diphosphothymidine
 >gi|230745|pdb|2SNM| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Val 66 Replaced By Lys (V66k)
 >gi|576398|pdb|2ENB| Staphylococcal Nuclease (E.C.3.1.31.1) Mutation With Asp 21 Replaced By Glu (D21e) Complexed With The Inhibitor Thymidine 3',5'-Diphosphate
 >gi|443374|pdb|2DTB| Delta-Toxin (Delta-Haemolysin) (Nmr, 9 Structures)
 >gi|1421454|pdb|1ZER| Mol_id: 1; Molecule: Histidine-Containing Phosphocarrier Protein; Chain: Null; Synonym: Hpr
 >gi|576294|pdb|1SYG| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Ala (P117a)
 >gi|576293|pdb|1SYF| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Thr (P117t) Complexed With 2'-Deoxy-3'-5'-Diphosphothymidine And Calcium
 >gi|576292|pdb|1SYE| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Thr (P117t)
 >gi|576291|pdb|1SYD| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Gly (P117g) Complexed With 2'-Deoxy-3'-5'-Diphosphothymidine And Calcium
 >gi|576290|pdb|1SYC| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Pro 117 Replaced By Gly (P117g)
 >gi|576289|pdb|1SYB| Staphylococcal Nuclease (E.C.3.1.31.1) With Residues 27 - 31 (Tyr-Lys-Gly-Gln-Pro) Replaced With Residues 160 - 165 Of Concanavalin A (Ser-Ser-Asn-Gly-Ser-Pro) Complexed With 2'-Deoxy-3'-5'-Diphosphothymidine And Calcium
 >gi|349914|pdb|1STY| Staphylococcal Nuclease (E.C.3.1.31.1) Insertion Mutant With Glycine Residue Inserted In An Alpha Helix, Between Arg126 And Lys127 (I26gI27) Complex With Calcium And Inhibitor Thymidine 3',5'-Bisphosphate
 >gi|999674|pdb|1STH| Staphylococcal Nuclease (E.C.3.1.31.1) Complexed With Co(II) Ion And Thymidine 3',5'-Bisphosphate (PdtP)
 >gi|999672|pdb|1STG| Staphylococcal Nuclease (E.C.3.1.31.1)
 >gi|576287|pdb|1STN| Staphylococcal Nuclease (E.C.3.1.31.1)
 >gi|576286|pdb|1STB| Staphylococcal Nuclease (E.C.3.1.31.1) Insertion Mutant With Leu Inserted At The End Of The Third Beta-Strand Between Leu 36 And Leu 37 (Ins(L36-L)) Complexed With Thymidine 3',5'-Diphosphate And Calcium
 >gi|576285|pdb|1STA| Staphylococcal Nuclease (E.C.3.1.31.1) Double Insertion Mutant With Two Glycine Residues Inserted In The First Beta Strand Between Pro 11 And Ala 12 (Ins(P11-Gg)) Complexed With Calcium And The Inhibitor Thymidine 3',5'-Diphosphate
 >gi|230332|pdb|1LSN| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant (Glu 43 Replaced By Asp) (E43D) Complex With A Calcium Ion And 3-Prime, 5-Prime-Deoxythymidine Bisphosphate
 >gi|230331|pdb|1SNC| Staphylococcal Nuclease (E.C.3.1.31.1) Complex With A Calcium Ion And 3-Prime, 5-Prime-Deoxythymidine Bisphosphate
 >gi|1431686|pdb|1PIO|B Chain B, Mol_id: 1; Molecule: Beta-Lactamase; Chain: A, B; Synonym: Penicillinase; Ec: 3.5.2.6; Engineered: Yes; Mutation: Ins(Met 30), A238s, Del(I239)
 >gi|1431685|pdb|1PIO|A Chain A, Mol_id: 1; Molecule: Beta-Lactamase; Chain: A, B; Synonym: Penicillinase; Ec: 3.5.2.6; Engineered: Yes; Mutation: Ins(Met 30), A238s, Del(I239)
 >gi|1127093|pdb|1NSN|S Chain S, Immunoglobulin, Staphylococcal Nuclease Mol_id: 1; Molecule: IgG Fab (IgG1, Kappa); Chain: L, H; Domain: Fragment N10; Synonym: N10 Fab Immunoglobulin; Mol_id: 2; Molecule: Staphylococcal Nuclease; Chain: S; Synonym: Staphylococcal Nuclease Ribonuclease, (Deoxyribonuclease)-3'-Nucleotidohydrolase; Ec: 3.1.31.1; Engineered: Yes
 >gi|999581|pdb|1KDC| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Lys 116 Replaced By Asn (K116n)
 >gi|999578|pdb|1KDB| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Lys 116 Replaced By Glu (K116e)
 >gi|999577|pdb|1KDA| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Lys 116 Replaced By Asp (K116d)
 >gi|640137|pdb|1KAN|B Chain B, Kanamycin Nucleotidyltransferase (E.C.2.7.7.-) Mutant With Asp 80 Replaced By Tyr And Thr 130 Replaced By Lys (D80y,T130k)
 >gi|640136|pdb|1KAN|A Chain A, Kanamycin Nucleotidyltransferase (E.C.2.7.7.-) Mutant With Asp 80 Replaced By Tyr And Thr 130 Replaced By Lys (D80y,T130k)
 >gi|494228|pdb|1KAB| Staphylococcal Nuclease (E.C.3.1.33.1) Mutant With Lys 116 Replaced By Gly (K116g)
 >gi|494227|pdb|1KAA| Staphylococcal Nuclease (E.C.3.1.33.1) Mutant With Lys 116 Replaced By Ala (K116a)

>gi|229907|pdb|1FC2|C Chain C, Immunoglobulin Fc And Fragment B Of Protein A Complex
 >gi|576100|pdb|1ENC| Staphylococcal Nuclease (E.C.3.1.31.1) Mutant With Asp 21 Replaced By Glu (D21e) Complexed With A Calcium Ion And The Inhibitor Thymidine 3',5'-Diphosphate
 >gi|576099|pdb|1ENA| Staphylococcal Nuclease (E.C.3.1.31.1) Mutation With Asp 21 Replaced By Glu (D21e) Complexed With A Calcium Ion
 >gi|442844|pdb|1DTC| Acetyl-Delta-Toxin (Acetyl-Delta-Haemolysin) (Nmr, 12 Structures)
 >gi|640251|pdb|1BLH| Beta-Lactamase (E.C.3.5.2.6) Complexed With [[n-(Benzyloxycarbonyl)amino]methyl]phosphonate
 >gi|515092|pdb|1BLP| Beta-Lactamase (E.C.3.5.2.6) P54 Mutant With Asp 179 Replaced By Asn (D179n)
 >gi|493890|pdb|1BLC| Beta-Lactamase (E.C.3.5.2.6) Complex With Degradation Products Of Clavulanate
 >gi|3152725|gb|AAC17130.1| enolase [Staphylococcus aureus]
 >gi|2463563|dbj|BAA22556.1| MURD [Staphylococcus aureus]
 >gi|2463562|dbj|BAA22555.1| MRAY [Staphylococcus aureus]
 >gi|2463561|dbj|BAA22554.1| penicillin-binding protein 1 [Staphylococcus aureus]
 >gi|2463560|dbj|BAA22553.1| unnamed protein product [Staphylococcus aureus]
 >gi|2463559|dbj|BAA22552.1| unnamed protein product [Staphylococcus aureus]
 >gi|1835218|emb|CAA71057.1| seryl-trna synthetase [Staphylococcus aureus]
 >gi|3122772|sp|O31203|RRF1_STAAU PROBABLE RIBOSOME RECYCLING FACTOR (RIBOSOME RELEASING FACTOR) (RRF)
 >gi|1488695|gb|AAC12901.1| novel antigen; orf-2 [Staphylococcus aureus]
 >gi|2826896|dbj|BAA24572.1| RecG [Staphylococcus aureus]
 >gi|2791991|emb|CAA74380.1| putative transposase [Staphylococcus aureus]
 >gi|2791990|emb|CAA74379.1| hypothetical protein [Staphylococcus aureus]
 >gi|2791989|emb|CAA74378.1| hypothetical protein [Staphylococcus aureus]
 >gi|2791988|emb|CAA74377.1| hypothetical protein [Staphylococcus aureus]
 >gi|2791987|emb|CAA74376.1| PBP2A [Staphylococcus aureus]
 >gi|2791986|emb|CAA74375.1| MecR1 protein [Staphylococcus aureus]
 >gi|2791985|emb|CAA74374.1| MecI protein [Staphylococcus aureus]
 >gi|2791984|emb|CAA74373.1| putative repressor [Staphylococcus aureus]
 >gi|2769708|gb|AAB95639.1| pristinamycin resistance protein VgaB [Staphylococcus aureus]
 >gi|2736228|gb|AAB94106.1| transducer protein [Staphylococcus aureus]
 >gi|2736227|gb|AAB94105.1| mutant sensor protein [Staphylococcus aureus]
 >gi|2736226|gb|AAB94104.1| pre-pheromone [Staphylococcus aureus]
 >gi|2736225|gb|AAB94103.1| signal transduction protein [Staphylococcus aureus]
 >gi|2736223|gb|AAB94102.1| transducer protein [Staphylococcus aureus]
 >gi|2736222|gb|AAB94101.1| mutant sensor protein [Staphylococcus aureus]
 >gi|2736221|gb|AAB94100.1| pre-pheromone [Staphylococcus aureus]
 >gi|2736220|gb|AAB94099.1| signal transduction protein [Staphylococcus aureus]
 >gi|2736218|gb|AAB94098.1| transducer protein [Staphylococcus aureus]
 >gi|2736217|gb|AAB94097.1| mutant sensor protein [Staphylococcus aureus]
 >gi|2736216|gb|AAB94096.1| pre-pheromone [Staphylococcus aureus]
 >gi|2736215|gb|AAB94095.1| signal transduction protein [Staphylococcus aureus]
 >gi|2696796|dbj|BAA24012.1| Fmt [Staphylococcus aureus]
 >gi|2696713|dbj|BAA24009.1| integrase [Staphylococcus aureus]
 >gi|2696712|dbj|BAA24008.1| LukF-PV [Staphylococcus aureus]
 >gi|2696711|dbj|BAA24007.1| LukS-PV [Staphylococcus aureus]
 >gi|216977|dbj|BAA00126.1| staphylocoagulase precursor [Staphylococcus aureus]
 >gi|773396|emb|CAA39963.1| QacA protein [Staphylococcus aureus]
 >gi|46660|emb|CAA39962.1| ORF188, has identity with known regulators such as tet regulator in Tn10 [Staphylococcus aureus]
 >gi|2645713|gb|AAB87473.1| ribosome recycling factor [Staphylococcus aureus]
 >gi|2641998|dbj|BAA23610.1| lipophilic protein [Staphylococcus aureus]
 >gi|2580436|dbj|BAA23141.1| histidyl-tRNA synthetase [Staphylococcus aureus]
 >gi|2580435|dbj|BAA23140.1| N-acetylmuramoyl-L-alanine amidase [Staphylococcus aureus]
 >gi|2580434|dbj|BAA23139.1| ORF1 [Staphylococcus aureus]
 >gi|2580433|dbj|BAA23138.1| ppGpp hydrolase [Staphylococcus aureus]
 >gi|2580432|dbj|BAA23137.1| adenine phosphoribosyltransferase [Staphylococcus aureus]
 >gi|1575062|gb|AAB81288.1| lytS [Staphylococcus aureus]
 >gi|1575061|gb|AAB81287.1| ScdA [Staphylococcus aureus]
 >gi|1694677|dbj|BAA13755.1| DnaA [Staphylococcus aureus]
 >gi|2506163|gb|AAB81232.1| AgrD [Staphylococcus aureus]
 >gi|1916240|gb|AAB81231.1| AgrA [Staphylococcus aureus]
 >gi|1916239|gb|AAB81230.1| AgrC-31 [Staphylococcus aureus]
 >gi|1916238|gb|AAB81229.1| AgrB [Staphylococcus aureus]
 >gi|2506165|gb|AAB80783.1| AgrD [Staphylococcus aureus]
 >gi|2506164|gb|AAB80779.1| AgrD [Staphylococcus aureus]
 >gi|1916248|gb|AAB80782.1| AgrA [Staphylococcus aureus]
 >gi|1916247|gb|AAB80781.1| AgrC [Staphylococcus aureus]
 >gi|1916246|gb|AAB80780.1| AgrB [Staphylococcus aureus]
 >gi|1916244|gb|AAB80778.1| AgrA [Staphylococcus aureus]
 >gi|1916243|gb|AAB80777.1| AgrC [Staphylococcus aureus]

>gi|1916242|gb|AAB80776.1| AgrB [Staphylococcus aureus]
 >gi|2344765|dbj|BAA21889.1| glutamic acid-specific protease [Staphylococcus aureus]
 >gi|2302281|emb|CAA03107.1| unnamed protein product [Staphylococcus aureus]
 >gi|2302279|emb|CAA03106.1| unnamed protein product [Staphylococcus aureus]
 >gi|2258300|gb|AAB63269.1| AgrC [Staphylococcus aureus]
 >gi|2258299|gb|AAB63268.1| AgrD [Staphylococcus aureus]
 >gi|2258298|gb|AAB63267.1| AgrB [Staphylococcus aureus]
 >gi|2258296|gb|AAB63266.1| AgrC [Staphylococcus aureus]
 >gi|2258295|gb|AAB63265.1| AgrD [Staphylococcus aureus]
 >gi|2258294|gb|AAB63264.1| AgrB [Staphylococcus aureus]
 >gi|2239274|gb|AAB62278.1| peptidoglycan hydrolase [Staphylococcus aureus]
 >gi|2224842|emb|CAA52098.1| squalene synthase [Staphylococcus aureus]
 >gi|2224841|emb|CAA52097.1| squalene desaturase [Staphylococcus aureus]
 >gi|437916|emb|CAA52296.1| isoleucyl-tRNA synthetase [Staphylococcus aureus]
 >gi|2190507|emb|CAA71446.1| outer surface binding 70kD protein [Staphylococcus aureus]
 >gi|153069|gb|AAB59090.1| sigma factor
 >gi|4433370|dbj|BAA22521.1| lipophilic protein which affects bacterial lysis rate and methicillin resistance level [Staphylococcus aureus]
 >gi|1262748|dbj|BAA12148.1| LukF-PV like component [Staphylococcus aureus]
 >gi|1230554|dbj|BAA12147.1| LukM component [Staphylococcus aureus]
 >gi|725454|dbj|BAA04185.1| autolysin [Staphylococcus aureus]
 >gi|725453|dbj|BAA04184.1| ORF3 [Staphylococcus aureus]
 >gi|725452|dbj|BAA04183.1| ORF2 [Staphylococcus aureus]
 >gi|725451|dbj|BAA04182.1| ORF1 [Staphylococcus aureus]
 >gi|540542|dbj|BAA01370.1| DNA gyrase A [Staphylococcus aureus]
 >gi|540541|dbj|BAA01369.1| DNA gyrase B [Staphylococcus aureus]
 >gi|522106|dbj|BAA06360.1| HSP40 [Staphylococcus aureus]
 >gi|487331|dbj|BAA06361.1| ORF35 [Staphylococcus aureus]
 >gi|487327|dbj|BAA06357.1| ORF37 [Staphylococcus aureus]
 >gi|441211|dbj|BAA06359.1| HSP70 [Staphylococcus aureus]
 >gi|441210|dbj|BAA06358.1| HSP20 [Staphylococcus aureus]
 >gi|441208|dbj|BAA03533.1| HSP60 [Staphylococcus aureus]
 >gi|441207|dbj|BAA03532.1| HSP10 [Staphylococcus aureus]
 >gi|216975|dbj|BAA14147.1| ORF for norA [Staphylococcus aureus]
 >gi|1483182|dbj|BAA13160.1| DNA polymerase III [Staphylococcus aureus]
 >gi|1777321|dbj|BAA11087.1| DNA topoisomerase IV GrlA subunit [Staphylococcus aureus]
 >gi|1777320|dbj|BAA11086.1| DNA topoisomerase IV GrlB subunit [Staphylococcus aureus]
 >gi|1777318|dbj|BAA11085.1| DNA topoisomerase IV GrlA subunit [Staphylococcus aureus]
 >gi|1777317|dbj|BAA11084.1| DNA topoisomerase IV GrlB subunit [Staphylococcus aureus]
 >gi|628920|pir||S40421| hypothetical protein - Staphylococcus aureus
 >gi|97848|pir||S12902| ricin chain A - Staphylococcus aureus
 >gi|97853|pir||S14180| transposase - Staphylococcus aureus (fragment)
 >gi|79909|pir||JU0116| transposase (insertion sequence IS431) - Staphylococcus aureus
 >gi|79889|pir||S00092| penicillin-binding protein - Staphylococcus aureus
 >gi|79872|pir||S04360| lacB protein - Staphylococcus aureus (fragment)
 >gi|628921|pir||S40422| hypothetical protein - Staphylococcus aureus
 >gi|1084186|pir||S54707| dnaA protein - Staphylococcus aureus
 >gi|628917|pir||S27240| enterotoxin B - Staphylococcus aureus (fragments)
 >gi|79852|pir||A29566| enterotoxin A - Staphylococcus aureus
 >gi|79850|pir||S02008| dihydrofolate reductase (EC 1.5.1.3) - Staphylococcus aureus (fragment)
 >gi|79845|pir||S15766| beta-hemolysin - Staphylococcus aureus
 >gi|97845|pir||C42295| recf protein - Staphylococcus aureus (fragment)
 >gi|2078390|gb|AAB54024.1| SecA [Staphylococcus aureus]
 >gi|2078382|gb|AAB54022.1| SecY [Staphylococcus aureus]
 >gi|2078381|gb|AAB54021.1| ribosomal protein L15 [Staphylococcus aureus]
 >gi|2078380|gb|AAB54020.1| ribosomal protein L30 [Staphylococcus aureus]
 >gi|2078378|gb|AAB54019.1| RplK; ribosomal protein L11 [Staphylococcus aureus]
 >gi|2078377|gb|AAB54018.1| NusG [Staphylococcus aureus]
 >gi|2078376|gb|AAB54017.1| SecE [Staphylococcus aureus]
 >gi|2058356|emb|CAB06539.1| dihydropteroate synthase [Staphylococcus aureus]
 >gi|1943995|dbj|BAA19494.1| sigA=sigma70 [Staphylococcus aureus]
 >gi|1943994|dbj|BAA19493.1| dnaG [Staphylococcus aureus]
 >gi|1943993|dbj|BAA19492.1| orf30 [Staphylococcus aureus]
 >gi|1943992|dbj|BAA19491.1| orf15 [Staphylococcus aureus]
 >gi|1934992|emb|CAA68933.1| ORF6 [Staphylococcus aureus]
 >gi|1934991|emb|CAA68932.1| sigma factor B [Staphylococcus aureus]
 >gi|1934990|emb|CAA68931.1| rsbW [Staphylococcus aureus]
 >gi|1934989|emb|CAA68930.1| rsbV [Staphylococcus aureus]
 >gi|1934988|emb|CAA68929.1| rsbU [Staphylococcus aureus]
 >gi|1934987|emb|CAA68928.1| ORF1 [Staphylococcus aureus]
 >gi|1916317|gb|AAB51152.1| alkyl hydroperoxide reductase subunit F [Staphylococcus aureus]

>gi|1916316|gb|AAB51151.1| alkyl hydroperoxide reductase subunit C [Staphylococcus aureus]
 >gi|1913907|gb|AAB51063.1| TagD [Staphylococcus aureus]
 >gi|1913906|gb|AAB51062.1| TagX [Staphylococcus aureus]
 >gi|1913905|gb|AAB51061.1| TagB [Staphylococcus aureus]
 >gi|1864022|gb|AAB50178.1| penicillin binding protein 4
 >gi|881631|gb|AAB50179.1| AbcA
 >gi|1657655|gb|AAB49445.1| Cap8P [Staphylococcus aureus]
 >gi|1657654|gb|AAB49444.1| Cap8O [Staphylococcus aureus]
 >gi|1657653|gb|AAB49443.1| Cap8N [Staphylococcus aureus]
 >gi|1657652|gb|AAB49442.1| Cap8M [Staphylococcus aureus]
 >gi|1657651|gb|AAB49441.1| Cap8L [Staphylococcus aureus]
 >gi|1657650|gb|AAB49440.1| Cap8K [Staphylococcus aureus]
 >gi|1657649|gb|AAB49439.1| Cap8J [Staphylococcus aureus]
 >gi|1657648|gb|AAB49438.1| Cap8I [Staphylococcus aureus]
 >gi|1657647|gb|AAB49437.1| Cap8H [Staphylococcus aureus]
 >gi|1657646|gb|AAB49436.1| Cap8G [Staphylococcus aureus]
 >gi|1657645|gb|AAB49435.1| Cap8F [Staphylococcus aureus]
 >gi|1657644|gb|AAB49434.1| Cap8E [Staphylococcus aureus]
 >gi|1657643|gb|AAB49433.1| Cap8D [Staphylococcus aureus]
 >gi|1657642|gb|AAB49432.1| Cap8C [Staphylococcus aureus]
 >gi|1657641|gb|AAB49431.1| Cap8B [Staphylococcus aureus]
 >gi|1657640|gb|AAB49430.1| Cap8A [Staphylococcus aureus]
 >gi|1854577|gb|AAB48183.1| lytR [Staphylococcus aureus]
 >gi|862312|gb|AAB48182.1| lytS [Staphylococcus aureus]
 >gi|1731452|gb|AAB48104.1| recombination protein [Staphylococcus aureus]
 >gi|1053003|gb|AAB48103.1| CAT protein [Staphylococcus aureus]
 >gi|1053002|gb|AAB48102.1| replication protein [Staphylococcus aureus]
 >gi|1848269|gb|AAB47993.1| quaternary ammonium compounds resistance protein Qac [Staphylococcus aureus]
 >gi|1848268|gb|AAB47992.1| replication protein Rep [Staphylococcus aureus]
 >gi|677847|emb|CAA24593.1| reading frame A [Staphylococcus aureus]
 >gi|677846|emb|CAA24590.1| reading frame C [Staphylococcus aureus]
 >gi|677845|emb|CAA24589.1| reading frame D [Staphylococcus aureus]
 >gi|677844|emb|CAA24588.1| reading frame E [Staphylococcus aureus]
 >gi|46746|emb|CAA38969.1| truncated alpha-toxin [Staphylococcus aureus]
 >gi|46559|emb|CAA24592.1| reading frame F transl. attenuator [Staphylococcus aureus]
 >gi|46558|emb|CAA24591.1| reading frame B mls resistance [Staphylococcus aureus]
 >gi|987499|gb|AAB41908.1| 5-dehydroquinase synthase
 >gi|987498|gb|AAB41907.1| chorismate synthase
 >gi|987497|gb|AAB41906.1| nucleoside diphosphate kinase
 >gi|987496|gb|AAB41905.1| geranylgeranyl pyrophosphate synthetase homolog; Method: conceptual translation supplied by author
 >gi|1262138|emb|CAA62900.1| glycerol 3-phosphate cytidyltransferase [Staphylococcus aureus]
 >gi|1262137|emb|CAA62899.1| penicillin-binding protein 4 [Staphylococcus aureus]
 >gi|1262136|emb|CAA62898.1| ATP-binding cassette transporter A [Staphylococcus aureus]
 >gi|1045529|gb|AAB39957.1| beta-lactamase
 >gi|1045527|gb|AAB39956.1| beta-lactamase
 >gi|1045525|gb|AAB39955.1| tetracycline resistance protein [Staphylococcus aureus]
 >gi|1045524|gb|AAB39954.1| replication protein [Staphylococcus aureus]
 >gi|1684749|emb|CAA70762.1| femD [Staphylococcus aureus]
 >gi|1204146|emb|CAA65106.1| fibronectin-binding protein [Staphylococcus aureus]
 >gi|1684751|emb|CAA70579.1| DNA directed RNA polymerase beta' chain [Staphylococcus aureus]
 >gi|1478385|gb|AAB36169.1| MsrSa=63 kda MsrA homolog (N-terminal) [Staphylococcus aureus, clinical isolate, pEP2104, Peptide Plasmid Partial, 31 aa]
 >gi|1042046|gb|AAB34958.1| IgG-binding polypeptide=protein A homolog [Staphylococcus aureus, strain 8325-4, Peptide Partial, 84 aa]
 >gi|999313|gb|AAB34910.1| 60 kda vitronectin-binding surface protein (N-terminal) [Staphylococcus aureus, prototype V8, Peptide Partial, 20 aa]
 >gi|998765|gb|AAB34258.1| enterotoxin H (N-terminal) [Staphylococcus aureus, FRI-569, Peptide Partial, 30 aa]
 >gi|894289|gb|AAB33482.1| alkaline shock protein 23, ASP23 [Staphylococcus aureus, 912, Peptide, 169 aa]
 >gi|619317|gb|AAB32218.1| beta-hemolysin, phospholipase C, PLC [Staphylococcus aureus, 126/89, Peptide, 331 aa]
 >gi|693735|gb|AAB31949.1| NorA (ISP794, quinolone resistance) [Staphylococcus aureus, NCTC 8325, Peptide Insertion, 388 aa]
 >gi|456770|gb|AAB28795.1| Tet(K)=tetracycline efflux protein [Staphylococcus aureus, pT181, Peptide Plasmid, 459 aa]
 >gi|433036|gb|AAB28599.1| adhesin (collagen binding domain) [Staphylococcus aureus, FDA 574, Peptide Partial, 37 aa]
 >gi|1680566|gb|AH004229.1| No definition line found

>gi|1680565|gb|AH004228.1| No definition line found
 >gi|299115|gb|AAB26122.1| gamma-hemolysin component II, H gamma II=leukocidin S homolog
 [Staphylococcus aureus, 4, RIMD 310925, Peptide Partial, 5 aa, segment 2 of 2]
 >gi|299114|gb|AAB26121.1| gamma-hemolysin component II, H gamma II=leukocidin S homolog
 [Staphylococcus aureus, 4, RIMD 310925, Peptide Partial, 58 aa, segment 1 of 2]
 >gi|299112|gb|AAB26120.1| gamma-hemolysin component I, H gamma I=leukocidin F homolog
 [Staphylococcus aureus, 4, RIMD 310925, Peptide Partial, 2 aa, segment 2 of 2]
 >gi|299111|gb|AAB26119.1| gamma-hemolysin component I, H gamma I=leukocidin F homolog
 [Staphylococcus aureus, 4, RIMD 310925, Peptide Partial, 59 aa, segment 1 of 2]
 >gi|265412|gb|AAB25337.1| V8 protease [Staphylococcus aureus, Peptide, 276 aa]
 >gi|248665|gb|AAB22051.1| chloramphenicol acetyltransferase, CAT (EC 2.3.1.28) [Staphylococcus
 aureus, 4.6 kb chloramphenicol resistance (CmR) plasmid pSCS6, Peptide Plasmid, 215 aa]
 >gi|246440|gb|AAB21603.1| 60 kda cell surface adhesin for heparan sulfate [Staphylococcus aureus,
 Peptide Partial, 4 aa]
 >gi|246439|gb|AAB21602.1| 66 kda cell surface adhesin for heparan sulfate [Staphylococcus aureus,
 Peptide Partial, 9 aa]
 >gi|239960|gb|AAB20545.1| 25-kda elastin-binding protein [Staphylococcus aureus, Peptide Partial, 14
 aa]
 >gi|239959|gb|AAB20544.1| 40-kda elastin-binding protein [Staphylococcus aureus, Peptide Partial, 18
 aa]
 >gi|1673527|gb|AAB18959.1| transposase [Staphylococcus aureus]
 >gi|1673525|gb|AAB18958.1| transposase [Staphylococcus aureus]
 >gi|1644433|gb|AAB17663.1| D-specific D-2-hydroxyacid dehydrogenase [Staphylococcus aureus]
 >gi|581567|emb|CAA37260.1| Sau96I DNA methyltransferase [Staphylococcus aureus]
 >gi|46618|emb|CAA37259.1| Sau96I restriction endonuclease [Staphylococcus aureus]
 >gi|46597|emb|CAA37902.1| transposase [Staphylococcus aureus]
 >gi|1587088|prf|2205353A pheromone [Staphylococcus aureus]
 >gi|1583755|prf|2121375A MHC class II-like protein [Staphylococcus aureus]
 >gi|229342|prf|710414A nuclease [Staphylococcus aureus]
 >gi|229233|prf|670719A nuclease [Staphylococcus aureus]
 >gi|1096955|prf|2113202C RNA polymerase:SUBUNIT=beta' [Staphylococcus aureus]
 >gi|1096954|prf|2113202B RNA polymerase:SUBUNIT=beta [Staphylococcus aureus]
 >gi|1096953|prf|2113202A ORF 202 [Staphylococcus aureus]
 >gi|1095875|prf|2110238A lipase [Staphylococcus aureus]
 >gi|1094971|prf|2107219C RNA polymerase:SUBUNIT=beta' [Staphylococcus aureus]
 >gi|1094970|prf|2107219B RNA polymerase:SUBUNIT=beta [Staphylococcus aureus]
 >gi|1094969|prf|2107219A rpoB upstream ORF [Staphylococcus aureus]
 >gi|1093504|prf|2104216A LukM protein [Staphylococcus aureus]
 >gi|1092377|prf|2023311A exotoxin [Staphylococcus aureus]
 >gi|742313|prf|2009360B pcrB protein [Staphylococcus aureus]
 >gi|742312|prf|2009360A helicase [Staphylococcus aureus]
 >gi|448909|prf|1918210C leukocidin [Staphylococcus aureus]
 >gi|448908|prf|1918210B leukocidin [Staphylococcus aureus]
 >gi|448907|prf|1918210A gamma hemolysin [Staphylococcus aureus]
 >gi|444424|prf|1907159A ethidium bromide resistance gene [Staphylococcus aureus]
 >gi|384172|prf|1905282A rep protein [Staphylococcus aureus]
 >gi|384170|prf|1905280A protein A [Staphylococcus aureus]
 >gi|383540|prf|1903261A toxic shock syndrome toxin [Staphylococcus aureus]
 >gi|228896|prf|1814271A Glu-C endoprotease [Staphylococcus aureus]
 >gi|228567|prf|1806229B repressor [Staphylococcus aureus]
 >gi|228566|prf|1806229A coinducer protein [Staphylococcus aureus]
 >gi|228100|prf|1717222A REP protein [Staphylococcus aureus]
 >gi|227968|prf|1714238A beta lactamase mutant S-3P [Staphylococcus aureus]
 >gi|227467|prf|1704203A enterotoxin A [Staphylococcus aureus]
 >gi|226860|prf|1609133A plasmid pOX1000 ORF A [Staphylococcus aureus]
 >gi|581544|emb|CAA27142.1| kanamycin nucleotidyltransferase (AA 1-253) [Staphylococcus aureus]
 >gi|46496|emb|CAA27141.1| repB polypeptide (AA 1-235) [Staphylococcus aureus]
 >gi|1245474|gb|AAB09712.1| nicking enzyme [Staphylococcus aureus]
 >gi|1586531|prf|2204232B penicillin-binding protein 4 [Staphylococcus aureus]
 >gi|1586530|prf|2204232A ABC transporter-like protein [Staphylococcus aureus]
 >gi|1585878|prf|2202209C ORF 3 [Staphylococcus aureus]
 >gi|1585877|prf|2202209B ORF 2 [Staphylococcus aureus]
 >gi|1585876|prf|2202209A ORF 1 [Staphylococcus aureus]
 >gi|1053140|gb|AAB09660.1| tetracycline resistance protein [Staphylococcus aureus]
 >gi|1575125|gb|AAB09464.1| beta-lactamase
 >gi|226340|prf|1507213A transposase, insertion seq IS257 [Staphylococcus aureus]
 >gi|225999|prf|1405331D repE gene [Staphylococcus aureus]
 >gi|225998|prf|1405331C ORF D [Staphylococcus aureus]
 >gi|225997|prf|1405331B rlx gene [Staphylococcus aureus]
 >gi|359739|prf|1313299A staphylocoagulase [Staphylococcus aureus]
 >gi|225442|prf|1303274B gene B [Staphylococcus aureus]

>gi|224810|prf||1202257F ORF [Staphylococcus aureus]
 >gi|224809|prf||1202257E gene tnpC [Staphylococcus aureus]
 >gi|224808|prf||1202257D gene tnpB [Staphylococcus aureus]
 >gi|224806|prf||1202257B gene spc [Staphylococcus aureus]
 >gi|224805|prf||1202257A gene ermA [Staphylococcus aureus]
 >gi|1567208|emb|CAA02065.1| Ble [Staphylococcus aureus]
 >gi|860732|gb|AAB07805.1| phosphoenolpyruvate carboxykinase [Staphylococcus aureus]
 >gi|1272327|gb|AAB07765.1| 3'5'-aminoglycoside phosphotransferase [Staphylococcus aureus]
 >gi|1272326|gb|AAB07764.1| truncated streptothricin acetyl transferase [Staphylococcus aureus]
 >gi|1236640|gb|AAB07747.1| multidrug resistance protein [Staphylococcus aureus]
 >gi|1236639|gb|AAB07746.1| partial duplication of the qacC gene [Staphylococcus aureus]
 >gi|1236638|gb|AAB07745.1| replication protein [Staphylococcus aureus]
 >gi|1053000|gb|AAB07714.1| replication protein [Staphylococcus aureus]
 >gi|1052999|gb|AAB07713.1| recombination protein [Staphylococcus aureus]
 >gi|1052998|gb|AAB07712.1| tetracycline resistance protein [Staphylococcus aureus]
 >gi|1125687|emb|CAA60583.1| glycerol-3-phosphate cytidyltransferase [Staphylococcus aureus]
 >gi|1125686|emb|CAA60582.1| penicillin binding protein 4 [Staphylococcus aureus]
 >gi|1125685|emb|CAA60581.1| mdr [Staphylococcus aureus]
 >gi|1125683|emb|CAA60586.1| glycerol-3-phosphate cytidyltransferase [Staphylococcus aureus]
 >gi|1125682|emb|CAA60585.1| penicillin binding protein 4 [Staphylococcus aureus]
 >gi|1125681|emb|CAA60584.1| mdr [Staphylococcus aureus]
 >gi|1495791|emb|CAA61517.1| DNA-directed RNA polymerase [Staphylococcus aureus]
 >gi|758691|gb|AAB06195.1| enterotoxin D
 >gi|1480567|gb|AAB05743.1| protein A
 >gi|1477533|gb|AAB05396.1| sarA
 >gi|1477532|gb|AAB05395.1| ORF3
 >gi|225996|prf||1405331A str gene [Staphylococcus aureus]
 >gi|225995|prf||1405330A repM gene [Staphylococcus aureus]
 >gi|225821|prf||1314205A protein A [Staphylococcus aureus]
 >gi|225444|prf||1303274D gene D [Staphylococcus aureus]
 >gi|225443|prf||1303274C gene C [Staphylococcus aureus]
 >gi|225441|prf||1303274A gene A [Staphylococcus aureus]
 >gi|224812|prf||1202257H peptide 2 [Staphylococcus aureus]
 >gi|224811|prf||1202257G peptide 1 [Staphylococcus aureus]
 >gi|224807|prf||1202257C gene tnpA [Staphylococcus aureus]
 >gi|224650|prf||1109959A nuclease, staphylococcal [Staphylococcus aureus]
 >gi|223937|prf||1005204A hemolysin delta [Staphylococcus aureus]
 >gi|1408063|gb|AAB03636.1| methicillin-resistance protein
 >gi|295162|gb|AAB03637.1| unknown ORF1; putative
 >gi|1407784|gb|AAB03613.1| orf-1; novel antigen
 >gi|642270|emb|CAA88043.1| DNA polymerase III [Staphylococcus aureus]
 >gi|1311537|gb|AAB02113.1| cop protein
 >gi|153094|gb|AAB02114.1| resistance protein
 >gi|153092|gb|AAB02112.1| replication protein
 >gi|673492|emb|CAA24594.1| nuclease [Staphylococcus aureus]
 >gi|1340131|emb|CAA66627.1| ORF4 [Staphylococcus aureus]
 >gi|1340130|emb|CAA66626.1| ORF3 [Staphylococcus aureus]
 >gi|1340129|emb|CAA66625.1| ORF2 [Staphylococcus aureus]
 >gi|1340128|emb|CAA66624.1| ORF1 [Staphylococcus aureus]
 >gi|758303|emb|CAA24957.1| staphylokinase [Staphylococcus aureus]
 >gi|736295|emb|CAA27035.1| A protein [Staphylococcus aureus]
 >gi|581591|emb|CAA34491.1| beta-lactamase (AA 1-281) [Staphylococcus aureus]
 >gi|581590|emb|CAA36953.1| blaZ protein (AA 1-281) [Staphylococcus aureus]
 >gi|581589|emb|CAA36950.1| binL protein (AA 1-197) [Staphylococcus aureus]
 >gi|46765|emb|CAA25801.1| put. alpha-toxin precursor (aa -26 to 293) [Staphylococcus aureus]
 >gi|46759|emb|CAA36952.1| blaR1 protein (AA 1-585) [Staphylococcus aureus]
 >gi|46758|emb|CAA36951.1| blaI protein (AA 1-126) [Staphylococcus aureus]
 >gi|46756|emb|CAA36949.1| ORF480 (pot. transposase) (AA 1-480) [Staphylococcus aureus]
 >gi|46755|emb|CAA36948.1| ORF271 (pot. ATP-binding protein) (AA 1-271) [Staphylococcus aureus]
 >gi|46753|emb|CAA31652.1| transposase (AA 1-224) [Staphylococcus aureus]
 >gi|46752|emb|CAA31651.1| transposase (AA 1-224) [Staphylococcus aureus]
 >gi|46751|emb|CAA31650.1| ORF140 (AA 1-140) [Staphylococcus aureus]
 >gi|46750|emb|CAA31649.1| S1 DHFR (AA 1-161) [Staphylococcus aureus]
 >gi|46749|emb|CAA31648.1| thymidylate synthetase (AA 1-318) [Staphylococcus aureus]
 >gi|46748|emb|CAA31647.1| transposase (AA 1-224) [Staphylococcus aureus]
 >gi|758275|emb|CAA29822.1| sak42D staphylokinase [Staphylococcus aureus]
 >gi|581583|emb|CAA24596.1| protein A [Staphylococcus aureus]
 >gi|459257|emb|CAA83066.1| Potential membrane spanning protein [Staphylococcus aureus]
 >gi|459256|emb|CAA83065.1| Potential ABC transporter [Staphylococcus aureus]
 >gi|46737|emb|CAA34476.1| precursor polypeptide (AA -26 to 632) [Staphylococcus aureus]
 >gi|46691|emb|CAA43604.1| protein A [Staphylococcus aureus]

>gi|46687|emb|CAA68434.1| preproenzyme (AA -68 to 268) [Staphylococcus aureus]
 >gi|1070386|emb|CAA63689.1| phosphoenolpyruvate-protein phosphatase [Staphylococcus aureus]
 >gi|1070385|emb|CAA63688.1| histidin-containing protein [Staphylococcus aureus]
 >gi|677852|emb|CAA45513.1| DNA-directed RNA polymerase beta' chain [Staphylococcus aureus]
 >gi|677851|emb|CAA45512.1| DNA-directed RNA polymerase beta chain [Staphylococcus aureus]
 >gi|677850|emb|CAA45511.1| hypothetical protein [Staphylococcus aureus]
 >gi|677849|emb|CAA45510.1| ribosomal protein L7/L12 [Staphylococcus aureus]
 >gi|581571|emb|CAA43217.1| chlorAMPhenicol acetyltransferase [Staphylococcus aureus]
 >gi|551670|emb|CAA51251.1| lukS [Staphylococcus aureus]
 >gi|551669|emb|CAA51250.1| ORF [Staphylococcus aureus]
 >gi|288292|emb|CAA51252.1| leucocidin F [Staphylococcus aureus]
 >gi|46652|emb|CAA43218.1| chlorAMPhenicol acetyltransferase [Staphylococcus aureus]
 >gi|1333818|emb|CAA26369.1| pot. orfB (aa 1-92) (4557 is 2nd base in codon) [Staphylococcus aureus]
 >gi|1333817|emb|CAA26368.1| pot. orfA [Staphylococcus aureus]
 >gi|809754|emb|CAA26365.1| unidentified reading frame [Staphylococcus aureus]
 >gi|581570|emb|CAA41339.1| dihydrolipoamide acetyltransferase: subunit E2 [Staphylococcus aureus]
 >gi|581568|emb|CAA27733.1| beta-lactamase (aa 1-281) [Staphylococcus aureus]
 >gi|488529|emb|CAA45728.1| S component of leucocodin R [Staphylococcus aureus]
 >gi|483534|emb|CAA44177.1| penicillin-binding protein 2 [Staphylococcus aureus]
 >gi|295834|emb|CAA39320.1| ORF 154 [Staphylococcus aureus]
 >gi|48874|emb|CAA41340.1| dihydrolipoamide dehydrogenase: subunit E3 [Staphylococcus aureus]
 >gi|48872|emb|CAA41338.1| pyruvate dehydrogenase (lipoamide): subunit Elbeta [Staphylococcus aureus]
 >gi|46647|emb|CAA29842.1| ORF (repE) [Staphylococcus aureus]
 >gi|46646|emb|CAA29841.1| orfD [Staphylococcus aureus]
 >gi|46645|emb|CAA29840.1| ORF (rlx) [Staphylococcus aureus]
 >gi|46644|emb|CAA29839.1| ORF (str) [Staphylococcus aureus]
 >gi|46639|emb|CAA31314.1| ORF 1 (AA 1 - 330) [Staphylococcus aureus]
 >gi|46638|emb|CAA31313.1| ORF 2 (AA 1 - 236) [Staphylococcus aureus]
 >gi|46636|emb|CAA30291.1| RepM protein (AA 1 - 314) [Staphylococcus aureus]
 >gi|46632|emb|CAA26367.1| CAT gene (aa 1-215) [Staphylococcus aureus]
 >gi|46631|emb|CAA26366.1| repD (aa 1-311) [Staphylococcus aureus]
 >gi|46629|emb|CAA68684.1| penicillin-binding protein (AA 1-670) [Staphylococcus aureus]
 >gi|46622|emb|CAA42079.1| E.coli isoleucyl tRNA synthetase homologue [Staphylococcus aureus]
 >gi|46620|emb|CAA42080.1| E.coli isoleucyl tRNA synthetase homologue [Staphylococcus aureus]
 >gi|46611|emb|CAA36829.1| PBP2' (AA 1-668) [Staphylococcus aureus]
 >gi|46609|emb|CAA45729.1| F component of leucocodin R [Staphylococcus aureus]
 >gi|1134886|emb|CAA54030.1| glutamine synthetase [Staphylococcus aureus]
 >gi|581562|emb|CAA44726.1| fibronectin binding protein B [Staphylococcus aureus]
 >gi|550424|emb|CAA57278.1| hlgB-like ORF [Staphylococcus aureus]
 >gi|550423|emb|CAA57277.1| hlgC-like ORF [Staphylococcus aureus]
 >gi|550422|emb|CAA57276.1| hlgA-like ORF [Staphylococcus aureus]
 >gi|468509|emb|CAA54029.1| glutamine synthetase repressor [Staphylococcus aureus]
 >gi|468508|emb|CAA54028.1| ORF1 [Staphylococcus aureus]
 >gi|311976|emb|CAA50893.1| fibrinogen-binding protein [Staphylococcus aureus]
 >gi|311974|emb|CAA50892.1| fibrinogen-binding protein [Staphylococcus aureus]
 >gi|296396|emb|CAA50571.1| DNA gyrase [Staphylococcus aureus]
 >gi|296395|emb|CAA50570.1| DNA gyrase [Staphylococcus aureus]
 >gi|296394|emb|CAA50569.1| RecF [Staphylococcus aureus]
 >gi|48713|emb|CAA36830.1| orf145 [Staphylococcus aureus]
 >gi|46606|emb|CAA32936.1| lacD polypeptide (AA 1-326) [Staphylococcus aureus]
 >gi|46605|emb|CAA32935.1| lacC polypeptide (AA 1-310) [Staphylococcus aureus]
 >gi|46589|emb|CAA31770.1| ORF 2 (68 AA) (2187 is 2nd base in codon) [Staphylococcus aureus]
 >gi|46588|emb|CAA31769.1| beta-hemolysin (AA 1 - 330) [Staphylococcus aureus]
 >gi|46587|emb|CAA31768.1| ORF 1 (AA 1 - 121) (1 is 2nd base in codon) [Staphylococcus aureus]
 >gi|46582|emb|CAA35680.1| ORF 419 protein [Staphylococcus aureus]
 >gi|46581|emb|CAA35679.1| FemA protein [Staphylococcus aureus]
 >gi|46580|emb|CAA35678.1| trpA protein (AA at 1) [Staphylococcus aureus]
 >gi|46576|emb|CAA26883.1| Methylase (AA 1-11) (172 is 2nd base in codon) [Staphylococcus aureus]
 >gi|809753|emb|CAA26103.1| pot. reading frame C (aa 51-230) (1 is 3rd base in codon) [Staphylococcus aureus]
 >gi|736294|emb|CAA68826.1| transposase [Staphylococcus aureus]
 >gi|671632|emb|CAA78911.1| unknown [Staphylococcus aureus]
 >gi|581558|emb|CAA53189.1| isoleucyl tRNA synthetase [Staphylococcus aureus]
 >gi|438228|emb|CAA53191.1| ORF C [Staphylococcus aureus]
 >gi|438227|emb|CAA53190.1| ORF B [Staphylococcus aureus]
 >gi|49313|emb|CAA78910.1| dihydrofolate reductase [Staphylococcus aureus]
 >gi|49018|emb|CAA44472.1| ethidium bromide resistance protein [Staphylococcus aureus]
 >gi|49017|emb|CAA44471.1| ethidium bromide resistance protein [Staphylococcus aureus]
 >gi|46573|emb|CAA38227.1| ermC [Staphylococcus aureus]
 >gi|46571|emb|CAA35972.1| staphylococcal enterotoxin C3 [Staphylococcus aureus]

>gi|46567|emb|CAA29260.1| enterotoxin C1 precursor (AA -27 to 239) [Staphylococcus aureus]
 >gi|46561|emb|CAA33598.1| ethidium bromide resistance protein (AA 1-107) [Staphylococcus aureus]
 >gi|46554|emb|CAA68825.1| ORF 140 [Staphylococcus aureus]
 >gi|46553|emb|CAA68824.1| dihydrofolate reductase type S1 [Staphylococcus aureus]
 >gi|46552|emb|CAA68823.1| thymidylate synthase [Staphylococcus aureus]
 >gi|46550|emb|CAA26107.1| pot. reading-frame C (aa 1-90) (4555 is 2nd base in codon) [Staphylococcus aureus]
 >gi|46549|emb|CAA26106.1| pot. reading-frame A (aa 1-315) [Staphylococcus aureus]
 >gi|46548|emb|CAA26105.1| reading frame D (aa 1-215) chloramphenicol resistance (CAT) [Staphylococcus aureus]
 >gi|46547|emb|CAA26104.1| pot. reading-frame B (aa 1-311) pot. replication protein [Staphylococcus aureus]
 >gi|4379429|emb|CAA24584.1| reading frame C (replication) [Staphylococcus aureus]
 >gi|1333816|emb|CAA24587.1| reading frame D [Staphylococcus aureus]
 >gi|1333815|emb|CAA24585.1| reading frame A [Staphylococcus aureus]
 >gi|1333813|emb|CAA34365.1| binR product (no atg) [Staphylococcus aureus]
 >gi|806585|emb|CAA89212.1| superoxide dismutase [Staphylococcus aureus]
 >gi|581555|emb|CAA26630.1| unidentified reading frame put. function in cat regulation [Staphylococcus aureus]
 >gi|398182|emb|CAA34366.1| bin3 product [Staphylococcus aureus]
 >gi|397526|emb|CAA79304.1| clumping factor [Staphylococcus aureus]
 >gi|46540|emb|CAA35664.1| coagulase precursor [Staphylococcus aureus]
 >gi|46537|emb|CAA26631.1| chloramphenicol acetyltransferase [Staphylococcus aureus]
 >gi|46534|emb|CAA24586.1| CAT (chloramphenicol resistance) [Staphylococcus aureus]
 >gi|809610|emb|CAA01358.1| sau3AI M [Staphylococcus aureus]
 >gi|580669|emb|CAA01357.1| sau3AI R [Staphylococcus aureus]
 >gi|512508|emb|CAA01068.1| fibronectin binding protein [Staphylococcus aureus]
 >gi|512504|emb|CAA01067.1| fibronectin binding protein [Staphylococcus aureus]
 >gi|512502|emb|CAA01066.1| fibronectin binding protein [Staphylococcus aureus]
 >gi|512500|emb|CAA01065.1| fibronectin binding protein [Staphylococcus aureus]
 >gi|512498|emb|CAA01064.1| fibronectin binding protein [Staphylococcus aureus]
 >gi|512496|emb|CAA01063.1| fibronectin binding protein [Staphylococcus aureus]
 >gi|512493|emb|CAA01062.1| fibronectin binding protein [Staphylococcus aureus]
 >gi|512491|emb|CAA01061.1| fibronectin binding protein [Staphylococcus aureus]
 >gi|512489|emb|CAA01060.1| fibronectin binding protein [Staphylococcus aureus]
 >gi|512487|emb|CAA01059.1| fibronectin binding protein [Staphylococcus aureus]
 >gi|412259|emb|CAA00843.1| Arp 4 [Staphylococcus aureus]
 >gi|412214|emb|CAA00364.1| structural A protein [Staphylococcus aureus]
 >gi|412211|emb|CAA00363.1| structural A protein [Staphylococcus aureus]
 >gi|765073|gb|AAA99982.1| autolysin
 >gi|765072|gb|AAA99981.1| ORF3
 >gi|765071|gb|AAA99980.1| ORF2
 >gi|765070|gb|AAA99979.1| ORF1
 >gi|790573|gb|AAA99709.1| pyrrolidone carboxyl peptidase
 >gi|46602|emb|CAA37814.1| putative transposase (AA 1 - 224) [Staphylococcus aureus]
 >gi|153077|gb|AAA98349.1| vgh gene product
 >gi|581278|emb|CAA26967.1| ORF [Staphylococcus aureus]
 >gi|581277|emb|CAA26960.1| tnpA protein [Staphylococcus aureus]
 >gi|43733|emb|CAA26966.1| peptide 1 [Staphylococcus aureus]
 >gi|43732|emb|CAA26965.1| peptide L [Staphylococcus aureus]
 >gi|43731|emb|CAA26964.1| S-adenosyl-methionine dependent methylase [Staphylococcus aureus]
 >gi|43730|emb|CAA26963.1| adenylyltransferase AAD9 (spc) [Staphylococcus aureus]
 >gi|43729|emb|CAA26962.1| pot. tnpC protein [Staphylococcus aureus]
 >gi|43728|emb|CAA26961.1| pot. tnpB protein [Staphylococcus aureus]
 >gi|1255262|gb|AAA96060.1| phosphoenolpyruvate carboxykinase
 >gi|1255260|gb|AAA96059.1| o-succinylbenzoic acid (OSB) synthetase
 >gi|1255259|gb|AAA96058.1| o-succinylbenzoic acid (OSB) CoA ligase
 >gi|46698|emb|CAA26428.1| put. AAD(9) determinant (aa 1-260) [Staphylococcus aureus]
 >gi|46697|emb|CAA26427.1| 3' end of tnpC [Staphylococcus aureus]
 >gi|46591|emb|CAA43885.1| Sphingomyelinase [Staphylococcus aureus]
 >gi|1196899|gb|AAA88547.1| unknown protein
 >gi|153000|gb|AAA88550.1| enterotoxin B
 >gi|152949|gb|AAA88549.1| transposase
 >gi|152948|gb|AAA88548.1| aminoglycoside resistance protein
 >gi|152947|gb|AAA88546.1| transposase
 >gi|1181627|gb|AAA86871.1| VAT B
 >gi|1016770|gb|AAA86131.1| prolipoprotein diacylglycerol transferase
 >gi|705406|gb|AAA82984.1| hyaluronate lyase
 >gi|1020317|gb|AAA79506.1| S-adenosylmethionine synthetase
 >gi|458420|gb|AAA79365.1| proline permease homolog
 >gi|1015409|gb|AAA79055.1| Pre protein

>gi|1015408|gb|AAA79054.1| chloramphenicol acetyltransferase
 >gi|1015407|gb|AAA79053.1| cat leader peptide
 >gi|1015406|gb|AAA79052.1| replication initiation protein
 >gi|915308|gb|AAA74889.1| fibrinogen binding protein
 >gi|409241|gb|AAA74375.1| penicillin-binding protein 2
 >gi|153086|gb|AAA73952.1| DNA gyrase A subunit
 >gi|153085|gb|AAA73951.1| DNA gyrase B subunit
 >gi|153084|gb|AAA73950.1| homologue; putative
 >gi|153062|gb|AAA72091.1| helicase
 >gi|153061|gb|AAA72090.1| [pcrA] gene products
 >gi|152957|gb|AAA71898.1| 5-enolpyruvylshikimate-3-phosphate synthase
 >gi|152956|gb|AAA71897.1| 3-phosphoshikimate-1-carboxyvinyltransferase
 >gi|152955|gb|AAA71896.1| 3-dehydroquinate synthase
 >gi|845687|gb|AAA67855.1| lacA repressor, putative
 >gi|845686|gb|AAA67853.1| ORF-27
 >gi|153035|gb|AAA67854.1| lacR repressor
 >gi|567036|gb|AAA64644.1| CapE
 >gi|506709|gb|AAA64652.1| CapM
 >gi|506708|gb|AAA64651.1| CapL
 >gi|506707|gb|AAA64650.1| CapK
 >gi|506706|gb|AAA64649.1| CapJ
 >gi|506705|gb|AAA64648.1| CapI
 >gi|506704|gb|AAA64647.1| CapH
 >gi|506703|gb|AAA64646.1| CapG
 >gi|506702|gb|AAA64645.1| CapF
 >gi|506700|gb|AAA64643.1| CapD
 >gi|506699|gb|AAA64642.1| CapC
 >gi|506698|gb|AAA64641.1| CapB
 >gi|506697|gb|AAA64640.1| CapA
 >gi|684950|gb|AAA62477.1| staphylococcal accessory regulator A
 >gi|567884|gb|AAA53114.1| lysyl-tRNA synthetase
 >gi|561880|gb|AAA53116.1| gyrase-like protein alpha subunit
 >gi|561879|gb|AAA53115.1| gyrase-like protein beta subunit
 >gi|463285|gb|AAA50463.1| putative
 >gi|551992|gb|AAA26680.1| 25 kD protein (putative); putative
 >gi|551991|gb|AAA26674.1| enterotoxin B
 >gi|495089|gb|AAA26675.1| recombinase
 >gi|398085|gb|AAA26683.1| acetyltransferase
 >gi|153125|gb|AAA26684.1| ATP-binding protein
 >gi|153123|gb|AAA26682.1| toxic shock syndrome toxin-1 precursor
 >gi|153121|gb|AAA26681.1| staphylococcal enterotoxin A precursor
 >gi|153115|gb|AAA26678.1| tetM
 >gi|153106|gb|AAA26677.1| protein A (ttg start codon)
 >gi|153104|gb|AAA26676.1| protein A (ttg start codon)
 >gi|153100|gb|AAA26673.1| Sau3AIM protein
 >gi|153099|gb|AAA26672.1| Sau3AIR protein (ttg start codon)
 >gi|153097|gb|AAA26671.1| bleomycin resistance protein
 >gi|153096|gb|AAA26670.1| neomycin resistance protein
 >gi|153090|gb|AAA26669.1| REP N protein (rep N)
 >gi|153088|gb|AAA26668.1| ethidium resistance protein (ebr)
 >gi|153082|gb|AAA26667.1| recombination and repair protein
 >gi|153080|gb|AAA26666.1| resistance protein
 >gi|153079|gb|AAA26665.1| transposase
 >gi|153067|gb|AAA26662.1| peptidoglycan hydrolase
 >gi|153057|gb|AAA26659.1| nuclease precursor
 >gi|153055|gb|AAA26658.1| norA
 >gi|537341|gb|AAA26647.1| beta-lactamase
 >gi|537340|gb|AAA26646.1| beta-lactamase
 >gi|537339|gb|AAA26645.1| beta-lactamase
 >gi|537338|gb|AAA26644.1| beta-lactamase
 >gi|537337|gb|AAA26643.1| beta-lactamase
 >gi|537336|gb|AAA26642.1| beta-lactamase
 >gi|475839|gb|AAA26654.1| leucocidin S component
 >gi|393266|gb|AAA26634.1| glycerol ester hydrolase
 >gi|295156|gb|AAA26639.1| gamma-hemolysin component B
 >gi|295155|gb|AAA26638.1| gamma-hemolysin component C
 >gi|295154|gb|AAA26637.1| gamma-hemolysin component A
 >gi|295152|gb|AAA26632.1| fibronectin-binding protein precursor
 >gi|153045|gb|AAA26653.1| prolipoprotein signal peptidase
 >gi|153041|gb|AAA26651.1| lincosaminide nucleotidyltransferase
 >gi|153039|gb|AAA26650.1| phospho-beta-galactosidase (lacG)

>gi|153038|gb|AAA26649.1| enzyme II-lac (lacE)
 >gi|153037|gb|AAA26648.1| enzyme III-lac (lacF)
 >gi|153033|gb|AAA26641.1| tagatose 6-phosphate isomerase
 >gi|153027|gb|AAA26640.1| DNA invertase (ttg start codon)
 >gi|153025|gb|AAA26636.1| gyrase A
 >gi|153024|gb|AAA26635.1| gyrase B
 >gi|153020|gb|AAA26633.1| lipase precursor (geh; EC 3.1.1.3)
 >gi|295151|gb|AAA26623.1| enterotoxin
 >gi|295149|gb|AAA26622.1| enterotoxin
 >gi|295147|gb|AAA26621.1| enterotoxin
 >gi|295145|gb|AAA26620.1| enterotoxin
 >gi|295143|gb|AAA26619.1| enterotoxin
 >gi|295141|gb|AAA26618.1| enterotoxin
 >gi|153012|gb|AAA26628.1| ETB precursor
 >gi|153008|gb|AAA26626.1| epidermolytic toxin A precursor
 >gi|153006|gb|AAA26625.1| ETA precursor
 >gi|153004|gb|AAA26624.1| enterotoxin C3
 >gi|153002|gb|AAA26617.1| enterotoxin type E precursor
 >gi|152998|gb|AAA26616.1| epidermal cell differentiation inhibitor
 >gi|152982|gb|AAA26613.1| chloramphenicol acetyltransferase
 >gi|152981|gb|AAA26612.1| precursor protein
 >gi|152979|gb|AAA26611.1| putative
 >gi|152978|gb|AAA26610.1| E1-E2 cadmium efflux adenosine triphosphatase
 >gi|152977|gb|AAA26609.1| cadmium resistance protein
 >gi|152976|gb|AAA26608.1| 125 codon reading frame that is similar to Tn554-encoded TnpC; RBS retained, but no evidence as to whether transcribed or expressed; putative
 >gi|152975|gb|AAA26607.1| 630 codon reading frame resembling tnpB of Tn554; transcription or translation signals upstream of the reading frame removed by the deletion noted above; presumed to be vestigial and not expressed; putative
 >gi|152974|gb|AAA26606.1| 29 codon reading frame of which N-terminal 25 are similar to the corresponding region of Tn554-encoded TnpA; TnpA is truncated by a 1006 bp deletion and is presumed inactive; putative
 >gi|152970|gb|AAA26605.1| beta-lactamase repressor
 >gi|152953|gb|AAA26598.1| alpha-hemolysin
 >gi|152951|gb|AAA26597.1| accessory gene regulator protein
 >gi|152945|gb|AAA26596.1| aminocyclitol-3'-phosphotransferase
 >gi|532967|gb|AAA21184.1| ORF
 >gi|295159|gb|AAA21183.1| putative
 >gi|295158|gb|AAA21182.1| mecR
 >gi|387880|gb|AAA20874.1| collagen adhesin
 >gi|310604|gb|AAA18516.1| ORF3
 >gi|310603|gb|AAA18515.1| ORF2
 >gi|310602|gb|AAA18514.1| ORF1
 >gi|409063|gb|AAA17490.1| exfoliative toxin A
 >gi|152985|gb|AAA16529.1| chloramphenicol acetyltransferase
 >gi|152984|gb|AAA16528.1| precursor protein
 >gi|458428|gb|AAA16512.1| FtsZ
 >gi|425478|gb|AAA16442.1| phosphatidylinositol-specific phospholipase C
 >gi|153053|gb|AAA16158.1| norA1199 protein

TABLE 7 : MAP AND SEQUENCE POSITION OF THE 73 ORFs PREDICTED TO BE ENCODED BY PHAGE 44AHJD THAT ARE GREATER THAN 33 AMINO ACIDS

Phage 44AHJD ORFs list

nb	Name	Frame	Position	Size (a.a.)	Key words
1	44AHJDORF001	-1	10342..12627	761	DNA polymerase;
2	44AHJDORF002	3	3789..5732	647	Techoic acid; Staph;
3	44AHJDORF003	2	6626..8389	587	Tail;
4	44AHJDORF004	1	8764..10227	487	Serine protease motif;
5	44AHJDORF005	-1	12643..13890	415	
6	44AHJDORF006	2	803..2029	408	
7	44AHJDORF007	1	2044..3027	327	Upper collar;
8	44AHJDORF008	2	3020..3775	251	Lower collar;
9	44AHJDORF009	2	5744..6496	250	Amidase; Staph;
10	44AHJDORF010	-2	13938..14420	160	
11	44AHJDORF012	3	8391..8813	140	Holin;
12	44AHJDORF013	-2	14586..14996	136	
13	44AHJDORF113	1	199..600	133	
14	44AHJDORF011	-2	15225..15593	122	
15	44AHJDORF114	-2	15870..16172	100	
16	44AHJDORF014	3	6243..6521	92	
17	44AHJDORF015	1	15403..15645	80	
18	44AHJDORF016	-1	15616..15852	78	
19	44AHJDORF017	-2	10536..10757	73	
20	44AHJDORF018	-1	886..1098	70	
21	44AHJDORF019	-2	9630..9836	68	
22	44AHJDORF121	-1	16165..16362	65	
23	44AHJDORF020	2	13865..14053	62	
24	44AHJDORF123	2	614..796	60	
25	44AHJDORF021	-2	5634..5816	60	
26	44AHJDORF023	-2	6315..6494	59	
27	44AHJDORF024	1	14275..14451	58	
28	44AHJDORF025	-3	14999..15175	58	
29	44AHJDORF026	-3	14426..14593	55	
30	44AHJDORF027	1	12916..13080	54	
31	44AHJDORF029	-1	15019..15183	54	
32	44AHJDORF028	-3	9071..9235	54	
33	44AHJDORF030	3	14487..14648	53	
34	44AHJDORF031	2	11039..11191	50	
35	44AHJDORF135	3	693..842	49	
36	44AHJDORF033	-1	3646..3795	49	
37	44AHJDORF032	-2	9306..9455	49	
38	44AHJDORF034	-3	14000..14146	48	
39	44AHJDORF035	-3	13811..13957	48	
40	44AHJDORF036	-3	10019..10165	48	
41	44AHJDORF022	-3	8468..8611	47	
42	44AHJDORF037	1	14788..14931	47	
43	44AHJDORF038	-2	3528..3671	47	
44	44AHJDORF039	3	1743..1883	46	
45	44AHJDORF040	2	9740..9877	45	
46	44AHJDORF041	2	15836..15973	45	
47	44AHJDORF042	-1	5014..5151	45	
48	44AHJDORF043	-1	4402..4539	45	
49	44AHJDORF044	-2	12783..12917	44	
50	44AHJDORF149	-2	639..770	43	
51	44AHJDORF046	1	4891..5019	42	
52	44AHJDORF047	1	11911..12039	42	
53	44AHJDORF045	2	10655..10783	42	
54	44AHJDORF048	-3	15212..15340	42	
55	44AHJDORF049	3	5784..5909	41	
56	44AHJDORF050	3	13158..13283	41	
57	44AHJDORF051	-2	10944..11066	40	
58	44AHJDORF052	-3	14216..14338	40	

59	44AHJDORF053	3	3348..3467	39	
60	44AHJDORF054	3	7551..7670	39	
61	44AHJDORF055	3	15705..15821	38	
62	44AHJDORF056	1	5512..5625	37	
63	44AHJDORF057	2	10121..10231	36	
64	44AHJDORF058	3	10767..10877	36	
65	44AHJDORF164	-1	592..702	36	
66	44AHJDORF059	-2	8250..8360	36	
67	44AHJDORF060	-2	6147..6257	36	
68	44AHJDORF061	2	15551..15658	35	
69	44AHJDORF062	1	4285..4389	34	
70	44AHJDORF063	-3	9383..9487	34	
71	44AHJDORF065	1	5029..5130	33	
72	44AHJDORF064	2	2609..2710	33	
73	44AHJDORF066	-2	10380..10481	33	

44AHJDORF001

44AHJDORF002

SD-138950.1

113 S A G L T S A F A L F K V T E M K Q M N D F K S E V K D
 4209 ttaattaaagattatgaccgtttcgtaaatgggtttgaattaaatgagcttgaaccaaagtttgatgggctttggtggtatt
 141 L I K D I D R F V N G F E L N E L E P K F V M G F G G I

 4293 cgcaacgcagtttaaccaatctattaattgataaagaacaaatcacatgtactctacacaatccgattctcaaaaaacctgaa
 169 R N A V N Q S I N I D K E T N H M Y S T Q S D S Q K P E
 4377 gggttttggataaataaattaacacctagtggtgacttaatttcaagcatgcgtattgtacagggtggtcatggtacaacaatc
 197 G F W I N K L T P S G D L I S S M R I V Q G G H G T T I
 4461 ggattagaacgtcaatccaatgggtgaaatgaaatctggttacatcacgatgggtgttgcaaaaactgttacaagtcgcatataaa
 225 G L E R Q S N G E M K I W L H H D G V A K L L Q V A Y K
 4545 gataattatgtattagatttagaagagggttaaggtttaacagattatacaccacagtcacttttaacaaacacacatttaca
 253 D N Y V L D L E E A K G L T D Y T P Q S L L N K H T F T
 4629 ccgttaatttgataagcaaatgacaaactcatttttaagattcggtgacggaacaataacaggttcgttcaagagcagacgtataaa
 281 P L I D E A N D K L I L R F G D G T I Q V R S R A D V K
 4713 aatcacattgataatgtagaaaaaagaatgacaattgataattcagaaaaaataatgataatcggttgatgcaaggcattgctggtt
 309 N H I D N V E K E M T I D N S E N N D N R W M Q G I A V
 4797 gatgtgatgatttatactggttaagtggttaacagttcagtttaattcacatggttcaaatcggttaaatcgttataacaaacaggt
 337 D G D D L Y W L S G N S S V N S H V Q I G K Y S L T T G
 4881 caaaagatttatgattatccatttaagttatcatatcaagacggtattaatttcccacgtgataactttaaagagcctgaggggt
 365 Q K I Y D Y P F K L S Y Q D G I N F P R D N F K E P E G
 4965 atttgctatttacaataacaaaaacaaaacgttaaatcggtattacttgctatgacaaaacggcggtggtggaacgtttccat
 393 I C I Y T N P K T K R K S L L L A M T N G G G K R F H
 5049 aatttatatgggtttctccaacttggtgagtgatgaacacttgaagcattacgcgcaagaggttcacaaaaactataaattaaca
 421 N L Y G F F Q L G E Y E H F E A L R A R G S Q N Y K L T
 5133 aaagacgcaggtcgctgctattctattccagaccattcagcagcttaaatgacttaacgcagcgtggtttatttattatgac
 449 K D D G R A L S I P D H I D D L N D L T Q A G F Y Y I D
 5217 ggggtgactgcagaaaaacttaagaatagccaatgaatgtagcaagcgtataattgacgctggttcttattatgataac
 477 G G T A A E K L K N M P M N G S K R I I D A G C F I N V Y
 5301 cctcaacacacaacttaggtacggttcaagaatttaacacagcttctcaacaggtcgtaaatgggtggtggtggtggtggtggtg
 505 P T T Q T L G T V Q E L T R F S T G R K M V K M V R G M
 5385 actttagacgtattttacgttaaaatgggattatggattatggacaacaatacaaaactgacgcaccatataagaatatttgga
 533 T L D V F T L K W D Y G L W T T I K T D A P Y Q E Y L E
 4569 gcaagtcataacaataactggtattgcttattgttaacaacagctgggtgagtgattacattacaggttaaccaaatgggaatttaga
 561 A S Q Y N N W I A Y V T T A G E Y Y I T G N Q M E L F R
 5553 gacgcgccagagaataaataaagtggtgcatggttacgtgtgtcaagtggttaacgcagtcggtgaagtaagacaacatta
 589 D A P E E I K K V G A W L R V S S G N A V G E V R Q T L
 5637 gaggtcaatatatacgaataataaagaattcttcagtaattgttaatgcggaacaaaacatcgtaattggttggttagcaaaa
 617 E A N I S E Y K E F F S N V N A E T K H R E Y G W V A K
 5721 catcaaaaatag 5732
 645 H Q K *

44AHJDORF003

6626 atgagaaagtttaacgaatttttaagtttttctataacacaccgtttacagactatcaaaacacagattcatttttaatagtaataaa
 1 M R K L T N F K F F Y N T P F T D Y Q N T I H F N S N K
 6710 gaacgtgatgatttttttaattggtcgtcgttaatttaattcgttagactattcaaaacacaggtataattttatcagtgataga
 29 E R D D Y F L N G R H F K S L D Y S K Q P Y N F I R D R
 6794 atggaaatcaatggtgatagcagtgccatgacgcacaaaggtattaactacatgacgtttttatcagattttgaggatagaaga
 57 M E I N V D M Q W H D A Q G I N Y M T F L S D F E D R R
 6878 tattacgctttgttaacaaaatcgaatacgtgaatgacgtgtgtgttaaaatataattttgtcattgataccattatgacgtat
 85 Y Y A F T V Q I E Y V N D V V V K I Y F V I D T I M T Y
 6962 acacaagggaatgtatttagagcaactctcaaacgtcaatattgaacgtcaacattttatcaaaacgcaggtataactatagtta
 113 T Q G N V L E Q L S N V N I E R Q H L S K R T Y N Y M L
 7046 ccaatgttacgttaataatgatgatgtgttaaaagtatacaataaaaaactatgtttataaccaaatgcaacaatatttggaat
 141 P M L R N N D D V L K V S N K N Y V Y N Q M Q Q Y L E N
 7130 ttagtattattccagtcgaagcgtgattttatcaagaaatttggtactaaaaagagccaaacttagatagcgtcaaaaggtacg
 169 L V L F Q S S A D L S K K F G T K K E P N L D T S K G T
 7214 atttatgacaatacacatcaccagtcacacttatcgttatggaataggtgactttattaactttatggataaaaatgagtggc
 197 I Y D N I T S P V N L Y V M E Y G D F I N F M D K M S A
 7298 tatccatggattacgcaaaactttcaaaaggttcaaatgttacctaagactttattaatacaaaaagacttagaggacgttaaa
 225 Y P W I T Q N F Q K V Q M L P K D F I N T K D L E D V K
 7382 accagtgaaaaaattacaggattaaaaacattaaaaacgggtggttaaatcaaaagaatggagtctaaaagatttatcattaagt
 253 T S K I T G L K T L D A G K S K E W S L K R T K S
 7466 ttctcaaatcttcaagagatgatgttatcaaaaaagatgaatttaaacatagatagcgaatgagtatatgacaattgaattt
 281 F S N L Q E M M L S K K D E F K H M I R N E Y M T I E F
 7550 tatgactgggaatggaataacgatgttactcgacgctggtaagattcacaaaaaactgggttaagttacgtacaaaatcaatt
 309 Y D N G N T M L L D A G K I T S Q K T G V K L R T K S
 7634 attgggttatcataatgaagttcgagtatatccagtagattataacagtgctgaaaaacgacagaccaataactcgctaaaaataaa
 337 I G Y H N E V R V Y P V D Y N S A E N D R P I L A K N K
 7718 gaaatattgattgacgggttcattcttaatacaaatataacatttaattagttttgcacaagttaccaatattaatcaataat
 365 E I L I T G S F L N T A T I T F N S F A Q I V P I L I N N
 7802 ggtatcttaggacaatcacacaagccaaccgacaaaaaatgcagaaagtcaatttaattacaaatcgatttgataatgtatta
 393 G I L G Q S Q Q A N R Q K N A E S Q L I T N R I D N V L
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7886 aatggtagcgaccgaaatcacgcttttatgacgctgtgagtgtagcaagtaatttaagtccaactgctttatttggttaagttt
421 N G S D P K S R F Y D A V S V A S N L S P T A L F G K F
7970 aatgaagaatataaatttctacaaacaacaagctgaatataaagatttagccttacaaccaccttctgtaactgaatcagaa
449 N E E Y N F Y K Q Q Q A E Y K D L A L Q P P S V T E S E
8054 atgggcaacgcattccaaattgcgaatagcatttaacgggtttaacgatgaaaatttagtgtagcgtcacctaaagaaattacattt
477 M G N A F Q I A N S I N G L T M K I S V P S P K E I T F
8138 ttacaaaaatatttatgtgtgtgtgtgtgaagtgaatgactataattcattttattgaaccaattaacagtagtactgtgtgc
505 L Q K Y Y M L F G F E V N D Y N S F I E P I N S M T V C
8222 aattattttaaagtgtacaggtacgtataactacvgtgacgtgcacccatgttaattggaacaaattaaagcaattttagaatct
533 N Y L K C T G T Y T I R D I D P M L M E Q L K A I L E S
8306 ggtgtaagattttggcataatgacggttcaggtaatccaatgttacaaaatcattaaataacaaatttagagaggggggtataa 8389
561 G V R F W H N D G S G N P M L Q N P L N N K F R E G V *

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8764 atgatactgaaaagagtgataacaatgaacgatcaagagaagatagataaatttacgcattcctatatattaatgatgattttggt
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8848 ttaacgatagaccagtttagtcctaaagtaaaaggatggcgcttttaattgtatggccttggtgggtaagaaagtaaaatcaga
29 L T I D Q L V P K V K G Y G R F N V W L G G N E S K I R
8932 caagtattaaaagcagtaaaagagatagggtgtttcacctactctttttgcccgtatatgaaaaaaatgagggttttagttctgga
57 Q V L K A V K E I G V S P T L F A V Y E K N E G F S S G
9016 ctgtgtgtgttaaacctacgtctgcacgtggtgattttaacagatgctaaattcatagcaagaaagtagtagtaccaca
85 L G W L N H T S A R G D Y L T D A K F I A R K L V S Q S
9100 aaacaagctggacaacgctcttggtatgacgcaggttaacatcgctccactttgtaccacaagacgtacaaagaaaggttaatgca
113 K Q A G Q P S W Y D A G N I V H F V P Q D V Q R K G N A
9184 gattttgcaaaaaatgaaagcaggtacaattgacgtgcatatattccattaacagcagctgctacttggcgccatattat
141 D F A K N M K A G T I G R A Y I P L T A A A T W A A Y Y
9268 ccttttaggtttgaaagcatcatatacaaaagtacaaaactatggtaatccatttttagacggtgcgaataactattctagcttgg
169 P L G L K A S Y N K V Q N Y G N P F L D G A N T I L A W
9352 ggtggttaattagacggttaaggtggatcacctagtgattctgctgacagtggttagtagtggtgacagtggttagtctactac
197 G G K L D G K G G S P S D S S D S G S S G D S G S L L
9436 gcttttagcaaaacaagccatgcaagaattattaaaaaaatacaagacgcattacaatgggacgttcatagtagtattggttagtga
225 A L A K Q A M Q E L L K K I Q D A L Q W D V H S I G S D
9520 aaatttttagtaattgattattttacattagaaaaaacattttaacacacatcatattaaaaatgacgattggtttacttgat
253 K F F S N D Y F T L E K T F N N T Y H I K M T I G L D
9604 tcattaaaaaaactgattgatagcgttcaagtagatagtgaggtagttagttctaactcctactgatgatgacggagaccataaa
281 S L K K L I D S V Q V D S G S S S S N P T D D D G D H K
9688 ccaattagtggttaaatcagtcagccaaatggaaaagtggtgctggtgattggtggttaactggacatagcacagttaccagaa
309 P I S G K S V K P N G K S G L G G N W T Y I G G N W T Y I P E
9772 aaatataaaaaagcaattggtgtacctttattcaaaaaagaataacttatatacaaacagggtaacatatttctcctcaaacgggta
337 K Y K K A I G V P L F K K E Y L Y K P G N I F P Q T G N
9856 gcaggacaattgacagaattaacatggcggtatgtcacactacatggttaaaagacaacctaccgacggtcaaatcaaca
365 A G Q C T E L T W A Y M S Q L H G K R Q P T D D G Q I T
9940 aacggctcagcgtgtatggtacgtctataaaaagtttaggtgcaaaaaacaacacataatccaacagtaggttatggtttctctagt
393 N G Q R V W Y V Y K K L G A K T T H N P T V G Y G F S S
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421 K P P Y L A T A Y G I G H T G V V V A V F E D G S F L
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449 V A N Y N V P P Y V A P S R V V L Y T L I N G V P N N A
10192 ggtgataatattgtattcttttagtggtattgcttaa 10227
477 G D N I V F F S G I A *

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13890 atggtaaaaacaaaatcggttttagacatggtaagagattatcaaatgctgtcaatcatgtcagaaaaaaaatcccagataagtat
1 M V K Q N R L D M V R D Y Q N A V N H V R K K I P D K Y
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29 N Q I E L V D E L M N D D I D Y Y I S I S N R S D G K S
13722 ttcaactatgtttcattttttatttttagctattaaacttgatataaaatttactttattatcacgtcattatacattacgt
57 F N Y V S F F I Y L A I K L D I K F T L L S R H Y T L R
13638 gacgcttaccgtgattttattgaagaaatcatagatgaaaatccactatttaaatcaaaacgtgtcacggtcagaagtgttagg
85 D A Y R D F I E E I I D E N P L F K S K R V T F R S A R
13554 gactatttagctattatctatcaagataaagaattggtgtgtattacagatttgaatagtgccactgattttaaataatcattct
113 D Y L A I I Y Q D K E I G V I T D L N S A T D L K Y H S
13470 aacttttttaaaacactatcctattattatattatgatgagtttttagcacttgaagatgattatttaattgatgagtggtgataag
141 N F L K H Y P I I I Y D E F L A L E D D Y L I D E W D K
13386 ttaaaaacaatatatgaatcaatcgaccgtaaacctggtaacgttgattatattggattccctaaaatggtttttactaggtaat
169 L K T I Y E S I D R N H G N V D Y I G F P K M F L L G N
13302 gcagtcacttttcaagtcctatattatccaatttaaatatatacaattttattacaaaagcataaaatgaatacatcaagactt
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13218 tacaaaaacatttttttagaaatgcgacgaaacgtaactgctgaatgaaaaacgtaacacacgtgcggttaattcaaatgacgac
225 Y K N E M R R N D Y V N E K R N T R A F N D
13134 gctatgacaactggagaatttgaatttaacgaatataattttggcggtatgataatttaagaaatcacatcaatcaaaacgggtgat
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13050 ttcttctatatcaaaactgatgataaatatattaaagtcattgtataatgtaactactttttatgacaaatattatcggtgtacca
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 12966 tatacaaaacaatatgaatgtttgtactaaaattagggatatagacaatcatgttacctatttacctgtgatgatgttttataaa
 309 Y T K Q Y E F C T K I R D I D N H V T Y L R D D M F Y K

12882 gaaaacatggaacgtttattactacaatccaagcaatttacattttgacaatgcttactctaaaaattacgtgggttgataatgat
 337 E N M E R Y Y Y N P S N L H F D N A Y S K N Y V V D N D
 12798 agatatttatatttagatatgaataaaaattataaaatttcataaaaaatgaaatgaagaaaaatatgagtgaagtttgaaaga
 365 R Y L Y L D M N K I I K F H I K N E M K K N M S E F E R
 12714 aaagaaaaatatacgaagataactatatagagaatacgaagaaagtatctaataaacaatatggcttataa 12643
 393 K E K I Y E D N Y I E N T K K Y L M K Q Y G L *

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 29 Y S K E Y T F G D K T V P I N M D L S K N E L M K R P
 971 aagattaatgagactttattaatcgatattgcattaggttaacgttttaattgggttagctaaagagcaagattttattggacaa
 57 K I N E T L L I D I A L G N R F N W L A K E Q D F I G Q
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 85 Y S E Y V I M D T V P I N M D L S K N E L M K R P
 1139 tatccacgtatggcaactaagttatattggtaacggaattgtgaagaacaaaaattcacattaacaacaatgatacagtttc
 113 Y P R M A T K L Y G N G I V K K Q K F T L N N N D T R F
 1223 aatttccaaacatttagcagacgcaactaattacgcttttaggtgtatcaaaaagaaaaatttctgatattaatgtattagaagaa
 141 N F Q T L A D A T N Y A L G V Y K K K I S D I N V L E E
 1307 aaagaaatgcgtgcaatgttagttgattactcattgaatcaattatccgaaacaaatgtacgtaaagcaacatcaaaagaagat
 169 K E M R A M L V D Y S L N Q L S E T N V R K A T S K E D
 1391 ttagcaagcaaaagttttgaagcaatcctaaacttacaacaaacagtgctaaatataatgaagtacatcgtgcattgaggtgt
 197 L A S K V F E A I L N L Q N N S A K Y N E V H R A S G G
 1475 gcaattggacaatatatacactgtatcaaaaattaaaagattttgtgatttttaacaacagattcattaaaattcttatcttttagat
 225 A I G Q Y T T V S K L K D I V I L T T D S L K S Y L L D
 1559 actaagattgcaaacacattccagattgcaggcattgattttcacagatcacgttattagttttgacgacttaggtggcggtgtt
 253 T K I A N T F Q I A G I D F T D H V I S F D D L G G V
 1643 aaagtaacaaaagatttaagttacaaaacaaagattcaattgactttttacgtgcgtatggagattatcaatcacaaattagga
 281 K V T K E F K L Q N Q D S I D F L R A Y G D Y Q S Q L G
 1727 gatacaattccagttgggtgctgtatttacttatgatgtatctaaacttaaaagagtttactggcaacgttgaagaaattaaacca
 309 D T I P V G A V F T Y D V S K L K E F T G N V E E I K P
 1811 aaatcagattttatgcgtttattttggatattaattcaaatataaaacgtttacacaaaaggtatgtttaaaccaccatttc
 337 K S D L Y A F I L D I N S I K Y K R Y T K G M L K P P F
 1895 cataacctgaatttgatgaagttacacactggattcattactattcatttaagccatttagtcatttcttaataaaatttta
 365 H N P E F D E V T H W I H Y Y S F K A I S P F F N K I L
 1979 attactgaccaagattgtaaatccaaacaggaagaattacaagaataa 2029
 393 I T D Q D V N P K P E E E L Q E *

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 2128 cgtcttatgtttaatcggttatttggaaattttaccgctactaatcaactataccaatcggtgatcgggttggtatagattttatt
 29 R L M F N R Y L E F L P L L I N Y T N R D T V G I D F I
 2212 cagttagaatcagctttaagacaaaacattaatgttagttgttggtgaagctagaataagcaaatattgattccttggttatgta
 57 Q L E S A L R Q N I N V V V G E A R N K Q I M I L G Y V
 2296 aataacacttactttaatcaagcaccacaaattttcatcaaaactttaatttccaatttcaaaaacgatttaactaaagaagatata
 85 N N T Y F N Q A P N F S S N F N F Q F Q K R L T K E D I
 2380 tattttattgtacctgactatttaatacctgtgattgtctacaaattcataagctatgataactgtatgagtggttaacttt
 113 Y F I V P D Y L I P D D C L Q I H K L Y D N C M S G N F
 2464 gttgtcatgcaaaataaaccattcaatataatagtgtatagaaattatagaacattatactgatgaattagcagaagttgct
 141 V V M Q N K P I Q Y N S D I E I I E H Y T D E L A E V A
 2548 ttatctcgcttttcttaatcatgcaagcaaaatttagcaagattttaaatcagaaattaatgacgagtcattcaatcaactt
 169 L S R F S L I M Q A K F S K I F K S E I N D E S I N Q L
 2632 gtgtccgaaatatataacggtgcaccatttgttaaaatgtcacctatgtttaatgcagatgacgatattcattgatttaacaagt
 197 V S E I Y N G A P F V K M S P M F N A D D D I I D L T S
 2716 aatagcgtatccagcatttaactgaaatgaaacggaatatcaaaacaaaatttagtgaattaagtaactatttaggcattaat
 225 N S V I P A L T E M K R E Y Q N K I S E L S N Y L G I N
 2800 tcattagccgttgataaagaaagcggtgtttcagacgaagaggcaaaaagttaacgtggatttaccacatcaaacagtaatatc
 253 S L A V D K E S G V S D E E A K S N R G F T T S N S N I
 2884 tattttaaagtcgtgaacaaattacgtttttatcaaagcgttatggttttagatattaaaccgtattacgatgataaacaacg
 281 Y L K G R E P I T F L S K R Y G L D I K P Y Y D D E T T
 2968 tctaaaatatcaatggttagacacactttttaagatgaaagcagtgatataaatggctag 3027
 309 S K I S M V D T L F K D E S S D I N G *

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3020 atggctagatacacaatgacttttatacgatttcattaatcagaattgattaaaaaagggtttcaatgaatttgtaaatgataat
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3104 aaattaacgtttttatgatgatgaatttcaattcatgcaaaaaatgctgaagttcgacaaagacgttttagctatcggttaataa
29 K L T F Y D D E F Q F M Q K M L K F D K D V L A I V N E
3188 aaagtatttaaagggtttttcattgaaagatgaattatcagatttactttttaaaaaatcatttacgattcatttttttagataga
57 K V F K G F S L K D E L S D L L F K K S F T I H F L D R
3272 gaaatcaacagacaaaacagttgaagcatttggcatgcaagtgattactgtattacacatgaggattattttaaattgtggtt
85 E I N R Q T V E A F G M Q V I T V C I T H E D Y L N V V
3356 tattcatcaagtgaagttgaaaaatactttacaatcacaaggcttcacagaacacaatgaagatacaacaagtaacactgatgaa
113 Y S S S E V E K Y L Q S Q G F T E H N E D T T S N T D E
3440 acatcgaatcaaaatgctacatcttttagacaattcaactggcatgactgcaaacagaaacgcttatgtgtcattaccacaaagt
141 T S N Q N A T S L D N S T G M T A N R N A Y V S L P Q S
3524 gaggttaacattgatgttgataatacaacgtttacgattcgctgataataatcagattgataacggttaaaactgtgaataaatcg
169 E V N I D V D N T T L R F A D N N T I D N G K T V N K S
3608 agtaacgaaagtaatacaaacgcaaacgtaatacaaaatcaaaaaggtaatacaaacggtacacaattcactaagcagttatta
197 S N E S N A K R G N A K G T Q F T K Q Y L
3692 attgataatattgataaagcgtacgatttaagaagaaaatttttaaatgaatttgataaaaaatgttttttcaaaaattggttag 3775
225 I D N I D K A Y D L R K K I L N E F D K K C F L Q I W *

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5744 atgaaatcacaacaacaagcaaaaagaatggatatataagcatgagggggcaggtgttgactttgatggtgcatatggatttcaa
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5828 tgtatggacttatcagttgcttatgtgtattactactgacggtaaaagttcgcatgtggggaatgctaaagacgcgataaat
29 C M D T S V A Y V Y I T D G K V R M W G N A K D A I N
5912 aatgacttttaaagggttttagcgacggtgtataaaaaatcacccgactttaaacctcaattaggggacgttgcgtatatacaaat
57 N D F K G L A T V Y K N T P S F K P Q L G D V A V Y T N
5996 ggacaataggacatattcaatgtgtgttaagtggaaatcttgattattatacatgcttagaacaacaaactgggttaggcggcggt
85 G Q Y G H I Q C V L S G N L D Y Y T C L E Q N W L G G G
6080 tttgacggttgggaaagcaaccatttagaacacattatttagcaggtgtgaactcattttattagacataaaattttcaggtagt
113 F D G W E K A T I R T H Y Y D G V T H F I R P K F S G S
6164 aatagcaaacgatttagaaacatcaaaagtaatacatttggaaaatggaaacgaaaccaatcggcgcacatttatagaatgaa
141 N S K A L E T S K V N T F G K W K R N Q Y G T Y Y R N E
6248 aatggtacatttaccatgtgtgttttttaccatatttgcacgtgtgcggttagtccaaaattatcagaacccaattggctattggttc
169 N G T F T C G F L P I F A R V G S P K L S E P N G Y W F
6332 caaccaaacggttatcacccatataacgaagtgtgtttatcagatggttacgtatggattggttataactggcaaggcacagct
197 Q P N G Y T P Y N E V C L S D G Y V W I G Y N W Q G T R
6416 tattatttaccagtgcccaatggaaatggaaaaacaggttaagttagttacagtggtgtgttcttgggggtttctcataa 6496
225 Y Y L P V R Q W N G K T G N S Y S V G I P W G V F S *

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14420 ttggttagacatacgtctgaaatggatagatggaaaaaagaagagaagctagaaaagagcaagaaaaagattttttttaaat
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14336 gatttttagtaattgtaatttttaatttgatgataaagatttacaagaggcgtagattgacacatggaaacattttgcacatctg
29 D F S N V N F K F D D K D L Q E A Y I D T W K H F A H L
14252 ccctattttcctaaagaaagaaacgtatcatatgtaaatgctgtatcattggttaagagggttaagacataaaaaattaaattat
57 P Y F P K E R N V S Y V N A V S L V R G S R H K K L N Y
14168 attcctgaaatatataacgcgaatgatgattcctaataaaaaacgctaaaaagcataaatacgttttatataatttacaagct
85 I L E I Y N R N D D S N N K N A K K H K Y A L Y N L Q A
14084 aaaaataataatttctcaatgtataaatatataaagaatcgatacttttatataaagaataatggtaaatcagatagacagtg
113 K N N N S S M Y K Y I K E I D T L Y K E I G K S D R P V
14000 acaaatattgatgatgaagatgtgaggtataactttttatattatgcaacatttgacgaataa 13938
141 T N I D D E D V R Y N F L Y Y A T F D E *

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15593 atgacaacgtaaaagatattttatcaagacaccaaacacattagcgagatttgaaatttgaggaaaaaagaagagaatttatc
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15509 aaactatcagaatttagtagaaaaatcgggtatgaaaaagagtatatcggttagagcattattcacaacaaagaatcaaaattc
29 K L S E L V E K Y G M K K E Y I V R A L F T N K E S K F
15425 ggtgaacaagggttatcgtcactgatgactataacgtaaaacttacggaaccacttaacagaattaattaaagaatgagagca
57 G E Q G V I V T D D Y N V N L P N H L T E L I K E M R A
15341 gatgaggacgttgttgacattatcaatgctggagaggttcaattcacaatttatgaatatgaaaacaaaaaagggtcaaaaagggt
85 D E D V V D I I N A G E V Q F T I Y E Y E N K K G Q K G
15257 tactcaatcaattttggtcaagtatcattttaa 15225
113 Y S I N F G Q V S F *

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8391 atgaacgaagtaaaattcagattttacagactcagaagcgtttcacatgttttatatcgcgtgggattttaaattactctacttt
1 M N E V K F R F T D S E A F H M F I Y A G D L K L L Y F
8475 ttatttgtattaatgttgcgttgatattatcaggttatcacaagcaattaaaaataataacttatggtcaaaaataatcaatg
29 L F V D I M F V D I T T G I S K A I K N N N L W S K K S M
8559 agaggattttctaaaaaattattgatattctgtattatcatttttagcaaacatcattgaccagattttacaattaaaagggtggt
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57 R G F S K K L L I F C I I I L A N I I D Q I L Q L K G G
8643 ctactcatgattacaatattttattatattgcaaatgagggactttctattgtagaaaattgtgcagaaatggacgtattagta
85 L L M I T I F Y I A N E G L S I V E N C A E M D V L V
8727 ccagacaataaagataaattaagagtcattaaaaatgatactgaaaagagtgtataacaatgaacgatcaagagaagataga
113 P E Q I K D K L R V I K N D T E K S D N N E R S R E D R
8811 taa 8813
141 *

44AHJDORF013

14996 atgaaaattaaaactacttttagattaaataatttaatttattaccttttaacaaatagagattattataatgataaatttgaa
1 M K I K T T F R L N N L I Y Y L L T N R D Y Y N D K F E
14912 aaatttactttcatctaataaaaaatgtatagtaaaaaataatgggtgtgtatattgagtttgacaaacaatatgatgat
29 K F T S S N K K C I V K I N M G D V Y I E F D K Q Y D D
14828 ttgaaattgaaaagagttattttagcttagatcgacattgatattaaaaaacatgttttaataacttgtattttattat
57 F E I E K E L F T L D I D I D I K K H V F N I L V F Y Y
14744 agaaattatttaagtaataagagaaatttataaactttacaattgacgacgtattatcaaattttgataaacct
85 R N Y L S N E L I R E I L L N V T I D D V L S N F D K P
14660 cttgaaagcgaattatgatttttatacaaaacaaagtcataacgataatgggaaagtgttgaccatgaataa 14586
113 L E S E L M I I Y Q N K V I Y D N G K V I D H E *

44AHJDORF113

199 atgacagaatttgatgaaatcgtaaaaccagacgacaaagaagaacttcagaatcaactgaagaaaatttagaatcaactgaa
1 M T E F D E I V K P D D K E E T S E S T E E N L E S T E
283 gaaacttcagaatcaactgaagaatcaactgaagaatcaactgaagataaaacagtagaacaactcgaagaa
29 E T S E S T E S T E S T E S T E S T E D K T V E T I E
367 gaaaatgaaaacaaatttagaacctactacaacagatgaagatagttcgaaatttgaccctgttgtattagaacaacgtattgct
57 E N E N K L E P T T T D E D S S K F D P V V L E Q R I A
451 tcttagaacaacaagtgtactactttttatcttcacaaatgcaacaaccacaacaagtacaacaacacaatcagatgtaaca
85 S L E Q Q V T T F L S S Q M Q Q P Q Q V Q Q T Q S D V T
535 gaatacaacaagaagataacgactattcagatgaagaactagttgataagtttagatttagattag 600
113 E S N K E D N D Y S D E E L V D K L D L D *

44AHJDORF114

16172 atgggttaattgtgataatgcaccagaagaaaaaggacagcctatactgaaatgttgcaactattcaataaactgattcaatgg
1 M V N V D N A P E E K G Q A Y T E M L Q L F N K L I Q W
16088 aatccagcttatacatttgacaatgcaattaacttattatcggtttgccaacaactattattaaactataatagttctgtgtgt
29 N P A Y T F D N A I N L S A C Q Q L L L N Y N S S V V
16004 caattcttaaatgatgaactaaacaacgaaactaaaccagaatcaatattgtcttataattgctggtgtatgacccaatagaacaa
57 Q F L N D E L N N E T K P E S I L S Y I A G D D P I E Q
15920 tggaatatgcataaaggattttatgaaacgtataacgtttacgttttttag 15870
85 W N M H K G F Y E T Y N V Y V F *

44AHJDORF014

6243 atgaaaatgggtacattttacatgtgggttttttaccatattttgcacgtgtcggttagtccaaaattatcagaacctaatggctatt
1 M K M V H L H V V F Y Q Y L H V S V V Q N Y Q N L M A I
6327 gggtccaacaaacgggttatacaccatataacgaagttgtttatcagatgggttacgtatggattgggtataactggcaaggca
29 G S N Q T V I H H I T K F V Y Q M V T Y G L V I T G K A
6411 cacgttattatttaccagtgcgccaatgggaatggaaaaacaggtaatagttacagtggttggtattccttgggggggtgttctcat
57 H V I I Y Q C A N G M E K Q V I V T V L V F L G G C S H
6495 aatgggtatttttagccttttttctttga 6521
85 N G Y F S L F L *

44AHJDORF015

15403 gtgacgataaacacctgtttcacogaattttgattctttgtttgtgaataatgctctaacgatatactcttttttataccgtat
1 V T I T P C S P N F D S L F V N N A L T I Y S F F I P Y
15487 ttttctactaattctgatagtttgataaattctctttcttttctctcaaatcaaatctcgctaattgtgttttggtgtcttgat
29 F S T N S D S L I N S L S F S S N S N L A N V F W C L D
15571 aaaatatctttttagcgtttgtcattttattttctcttattttaaattattgtctttctgcaattgcatgttag 15645
57 K I S F T F V I L F L L L F K L F A F C N C D L *

44AHJDORF016

15852 atgaaagttagcagacattgtttaccttacgtgtcaagggttatatacttcattacttagatgatgaataacattgaggaa
1 M K V D D I V T L R V K G Y I L H Y L D D D N E Y I E E
15768 tttttaccacttcacgagtatcatttaacaaaaacacaaagcaaaagaattattaccagacacatgtaaacattgtccactaca
29 F L P L H E Y H L T K T Q A K E L L P D T C K L L S T T
15684 cgcacaacgaaattcaagttttatacaatgattttactacaatcgcaattgcagaaagcaaat 15616
57 R T T K T I Q V Y Y N D L L Q I A I A E S K *

44AHJDORF017

10757 atggaaagattaaaattgcttctgctggtataccgaaaaacgcctttgatacaagcgtcgattttgaaacctttgtacgtgaac
1 M E R L K L L L L V Y R K T P L I Q A S I L K P L Y V N
10673 aattctttgacggtgcatatttgaaaacaataaaagtatctataatgagcaaggtacaatatcgatatatccgtctaaaactg
SD-138950.1

29 N S L T V P L L K T I K V S I M S K V Q Y R Y I R L K L
10589 aaattgtatgtggtaatgtatatgatgaatattttactgatgaacttaatatga 10536
57 K L Y V V M Y M M N I L L M N L I *

44AHJDORF018

1098 atgttaattggtactgtgtccataatcacgtattcttcactatattgtccaataaaatcttgctcttttagctaaccaattaaaa
1 M L I G T V S I I T Y S S L Y C P I K S C S L A N Q L K
1014 cgattacctaatacgcaatcgattaataaaagtctcattaatcttagggaataaatatttattacaaatgtttcgaacattgta
29 R L P N A I S I N K V S L I L G N K Y L F T N V S N I V
930 tttgaattatccatttgtcgccaaatgtccaagattttgaataa 886
57 F E L S H L S P N V Q D F E *

44AHJDORF019

9836 atgttacctggtttgtataagtattctttttgaataaaggtacaccaattgcttttttatattttcttggaactgtgcatat
1 M L P G L Y K Y S F L N K G T P I A F L Y F S G N C A Y
9752 gtccagttaccaccaatcacagaccactttttccatttggcttgactgatttaccactaattggtttatggctccgcatca
29 V Q L P P I T R P L F P F G L T D L P L I G L W S P S S
9668 tcagtaggattagaactactactccactatctacttga 9630
57 S V G L E L L L P L S T *

44AHJDORF121

16362 atggaaaatgaacaaaaaacattgagttgaagcatgtttttcgttttaagaatggaagtttatgtatagcgttatttgataga
1 M E N E T K N I E L K H V F R F K N G S L C I A L F D R
16278 acagaaaatgaatttcattttatgatgttgacattgatgaattgaagatttaaatcataattctgttttacgcgtaatttca
29 T E N E I S F Y D V D I D E I E D L N H N S V L R V I S
16194 actttattaggaagtataataatggttaa 16165
57 T L L G S D N N G *

44AHJDORF020

13865 atgtctaaacgattttgttttaaccatgtttttgctccttgtaaatagtttatgatgtcgtttacagtggttaatttattcgtcaa
1 M S K R F C F T M F L L L V I V Y D V V Y S V K F I R Q
13949 atgttgcataatataaaaagttataacctcacatcttcatcatcaatatttgtcactggcttatctgatttaccattttctttat
29 M L H N I K S Y T S H L H H Q Y L S L V Y L I Y Q F L Y
14033 ataaagtatcgattttcttttaa 14053
57 I K Y R F L *

44AHJDORF123

614 atgtatgagggaaacaacatgcgttctatgatgggtacatcatatgaagattcaagattaaataaacgaacagaattaaatgaa
1 M Y E G N N M R S M M G T S Y E D S R L N K R T E L N E
698 aacatgtcaattgatacaaaaaagtgaaagatagttatgggtgacaaattcattcactttcaaaaacatcatttacaggtgac
29 N M S I D T N K S E D S Y G V Q I H S L S K Q S F T G D
782 gttgaggaggaataa 796
57 V E E E *

44AHJDORF021

5816 atgcaccatcaaagtcacacacctgccccctcatgcttatatatccattcttttgcttggttggtgatttcatttatatcactc
1 M H H Q S Q H L P P H A Y I S I L L L V V V I S F I S L
5732 ctatttttgatgttttgctacccaacatattcacgatgttttgcttcgcattacattactgaagaattcttttatattccga
29 L F L M F C Y P T I F T M F C F R I N I T E E F F I F R
5648 tatattagcctctaa 5634
57 Y I S L *

44AHJDORF022

8611 atgtttgctaaaatgataatacagaatatcaataatttttttagaaaatcctctcattgatttttttgaccataagttattattt
1 M F A K M I I Q N I N N F L E N P L I D F F D H K L L F
8527 ttaattgcttttgaaatacctgtaataatatcaacgaacattaatacaaaaaaagtag 8468
29 L I A F E I P V I I S T N I N T N K K *

44AHJDORF023

6494 atgagaacaccccccaaggaataaccaacactgtaactattacctgtttttccattccattggcgactggtaataataaacgtg
1 M R T P P K E Y Q H C N Y Y L F F H S I G A L V N N N V
6410 tgccttgccagttataaccaatccatacgttaaccatctgataaacaacttcgtttatatgggtgtataaccgttttggttggaacc
29 C L A S Y N Q S I R N H L I N K L R Y M V Y N R L V G T
6326 aatagccattag 6315
57 N S H *

44AHJDORF024

14275 gtgtcaatgtacgcctcttgttaaattctttatcatcaaatttaaaattaacattactaaaaatcatttaaaaaataaatctttttct
1 V S M Y A S C K S L S S N L K L T L L K S F K N K S F S
14359 tgctctttttagcttctcttcttttttccatctatccatttcagacgtatgtctaaccaatgttatcaacctccatataaag
29 C S F L A S L S F F H L S I S D V C L T N V I N L H I K
14443 cataaataa 14451

57 H K *

44AHJDORF025

15175 atggaacgtaaatacaaaacggtattattatattgcatgagattaaaggacattttccacatcaaactcctcaatgtttgaagat
1 M E R K Y K T V L L Y C D E I K G H F P H Q I S M F E D
15091 ttatatgacgctaaagttgtatattcatattatgaatataacctgttcactaaaaataacgcgtatatcatagaatacattaag
29 L Y D A K V V Y S Y Y E Y N L F T K K Y A Y I I E Y I K
15007 gagatataa 14999
57 E I *

44AHJDORF026

14593 atgaataacctattaaacatagccattgttttcccttttagcatttttaattacacttatcatacttatgacactgcatatacgc
1 M N N L L N I A I V F L L A F L I T L I I L M T L H I R
14509 gtgtcatttgggtgttttattcactacattgattatattctatattatcttttaaatggttatttatgcttttatatggagggtga 14426
29 V S F G V L F T T L I I F Y I I F L M V I Y A L Y G G *

44AHJDORF027

12916 atgattgtctatccctaatttttagtacaaaattcatattgttttgtatatggtacaacgataaatatttgcataaaagtagt
1 M I V Y I P N F S T K F I L F C I W Y N D N I C H K S S
13000 tacattatacatgactttaatatatttatcatcagttttgatatagaagaatcacggttttgattgatgtgatttcttaa 13080
29 Y I I H D F N I F I I S F D I E E I T V L I D V I S *

44AHJDORF029

15183 gtgttttaaatggaacgtaaatacaaaacggtattattatattgcatgagattaaaggacattttccacatcaaactcctcaatgt
1 V F K W N V N T K R Y Y Y I A M R L K D I F H I K S Q C
15099 ttgaagatttatatgacgctaaagttgtatattcatattatgaatataacctgttcactaaaaataacgcgtatatcatag 15019
29 L K I Y M T L K L Y I H I M N I T C S L K N T R I S *

44AHJDORF028

9235 atggaatatatgcacgtccaattgtacctgctttcatatttttgcaaaatctgcattaccttttctttgtacgtcttggta
1 M E Y M H V Q L Y L L S Y F L Q N L H Y L F F V R L V V
9151 caaagtgacgatgttacctgcgtcataccaagacggtgtccagcttgttttgattgtgataacttttctgtatga 9071
29 Q S G R C Y L R H T K T V V Q L V L I V I L T F L L *

44AHJDORF030

14487 gtgaataaaacaccaaagacacgcgtatatgcagtgatcataagtgataagtgtaattaaaaatgctaaaaggaaaacaatg
1 V N K T P N D T R I C S V I S M I S V I K N A K R K T M
14571 gctatgttttaataggttattcatgtgcaatcactttccattatcgatatgactttgttttgataaataatcattaa 14648
29 A M F N R L F M V N H F P I I V Y D F V L I N N H *

44AHJDORF031

11039 atgatattgtatagttcattgtttatcatctaacggaataagttaaaatgtgaacgtaatgcaggtatgccatataatccattt
1 M I L Y S S L L S S K R N K L K C E R N A G M P Y N P F
11123 aaaacgacttttagataacataacctcctcatttgagtatgggtgttcggtgatatcatcagtaattgtga 11191
29 K T T L D N I T S S F E Y G C S L I S S V M *

44AHJDORF135

693 atgaaaacatgtcaattgatacaaaataaaagtgaagatagttatggtgtacaaattcattcactttcaaaacaatcatttacag
1 M K T C Q L I Q I K V M V Y K F I H F Q N N H L Q
777 gtgacgttgaggaggaataataaattatggcacaacaatctacaaaaaatgaaactgcacttttag 842
29 V T L R R N N K L W H N N L Q K M K L H F *

44AHJDORF033

3795 atgccattatttaaccacctctaccaaatttgtaaaaaacatttttatcaaattcatttaaaattttctttcttaaatcgtac
1 M P L F N H L Y Q I C K K H F L S N S F K I F F L K S Y
3711 gctttatcaatattatcaattaaatactgcttagtgaattgtgtaccttttgacattacctttttga 3646
29 A L S I L S I K Y C L V N C V P F A L P F *

44AHJDORF032

9455 atggcttgttttgctaaagcgagtagtgaactaccactgtcaccactactaccactgtcagacgaatcactaggtgatccacct
1 M A C F A K A S S E L P L S P L L P L S D E S L G D P P
9371 ttaccgtctaatttaccaccccaagctagaatagtattcgaccgtctaaaatggattaccatag 9306
29 L P S N L P P Q A R I V F A P S K N G L P *

44AHJDORF034

14146 atgatgattctaataataaaaaacgctaaaaagcataaatacgttttatataatttacaagctaaaaataataattcttcaatgt
1 M M I L I I K T L K S I N T L Y I I Y K L K I I I L Q C
14062 ataaatatattaaagaaatcgatactttatataaagaaattggtaaatcagatagaccagtga 14000
29 I N I L K K S I L Y I K K L V N Q I D Q *

44AHJDORF035

13957 atgcaacatttgacgaataaatttaacactgtaaacgacatcataaactattacaaggagcaaaaacatggtaaaacaaaatcg
1 M Q H L T N K F N T V N D I I N Y Y K E Q K H G K T K S
13873 tttagacatggtaagagattatcaaaatgctgtcaatcatgtcagaaaaaaatcccagataa 13811
29 F R H G K R L S K C C Q S C Q K K N P R *

44AHJDORF036

10165 gtgtatataataccacacgtgatgggtgcaacatatgggtgtacattatagtttgcaactaaaaacgaaccatcttcaaaaactg
1 V Y T I P H V M V Q H M V V H Y S L Q L K T N H L Q K L
10081 ctacaacaacacctgtgtgaccaataccatatgcagttgcttgaagtatgggtgtttactag 10019
29 L Q Q H L C D Q Y H M Q L L V S M V V Y *

44AHJDORF037

14788 atgtcgatatctaacgtaaataactctttttcaatttcaaaatcatcatattgtttgtcaaaactcaatatacacatcacccata
1 M S I S N V N N S F S I S K S S Y C L S N S I Y T S P I
14872 tttatttttactatacatctttttattagatgaagtaatttttcaaaatttatcattataa 14931
29 F I F T I H F L L D E V N F S N L S L *

44AHJDORF038

3671 gtgtaccttttgcattacctttttgattttgattacgttttgcgttttgattactttcgttactcgattttattcacagttttac
1 V Y L L H Y L F D F D Y V L R F D Y F R Y S I Y S Q F Y
3587 cgttatcaatcgattattatcagcgaatcgtaacgtttgtattatcaacatcaatgttaa 3528
29 R Y Q S Y Y Y Q R I V T L Y Y Q H Q C *

44AHJDORF039

1743 gtgctgtattttacttatgatgtatctaaacttaaagagtttactggcaacgttgaagaaattaaacaaaaatcagatttatatg
1 V L Y L L M M Y L N L K S L L A T L K K L N Q N Q I Y M
1827 cgtttattttggatattaattcaattaaatataaacggttacacaaaagggtatgttaa 1883
29 R L F W I L I Q L N I N V T Q K V C *

44AHJDORF040

9740 gtggtaactggacatatgcacagttaccagaaaaatataaaaaagcaattgggtgtaccttttattcaaaaaagaatacttataca
1 V V T G H M H S Y Q K N I K K Q L V Y L Y S K K N T Y T
9824 aaccaggttaacatatttctcctcaaacgggtaatgcaggacaatgtacagaattaa 9877
29 N Q V T Y F L K R V M Q D N V Q N *

44AHJDORF041

15836 atgtcgtcaacttttcattattatatcactccttttctaaaaaacgttaaacgtttatcgttttcataaaatccttttatgcatattcc
1 M S S T F I I I S L L S K K R K R Y T F H K I L Y A Y S
15920 attgttctattgggtcatcaccagcaatataagacaatattgattctggttttag 15973
29 I V L L G H H Q Q Y K T I L I L V *

44AHJDORF042

5151 atgcacgaccgtcgtctttttgttaatttatagttttgtgaacctcttgcgcgtaatgcttcaaagtgttcatactcaccaagtt
1 M H D R R L L I Y S F V N L R V M L Q S V H T H Q V
5067 ggaagaaacatatataaattatggaacgtttttccaccaccgcccgtttgtcatag 5014
29 G R N H I N Y G N V F H H R R L S *

44AHJDORF043

4539 atgcgacttgtaacagttttgcaacaccatcgtgatgtaaccagatttttcatttcaccattggattgacgtttctaatccgattg
1 M R L V T V L Q H H R D V T R F S F H H W I D V L I R L
4455 ttgtaccatgaccacctgtacaatcgcgatgcttgaaattaagtcaccactag 4402
29 L Y H D H P V Q Y A C L K L S H H *

44AHJDORF044

12917 atgttacctattttacgtgatgatgtttttataaagaaaacatggaacgttattactacaatccaagcaattttacattttgaca
1 M L P I Y V M I C F I K K T W N V I T T I Q A I Y I L T
12833 atgcttactctaaaaattacgtgggtgataatgatagattttatatttag 12783
29 M L T L K I T W L I M I D I Y I *

44AHJDORF149

770 atgattgtttttgaaagtgaatgaattttgtacaccataactatcttcactttttatttgatcaattgacatgttttcatttaatt
1 M I V L K V N E F V H H N Y L H F Y L Y Q L T C F H L I
686 ctgttcgtttattttatcttgaatcttcatatgatgtacccatcatag 639
29 L F V Y L I L N L H M M Y P S *

44AHJDORF046

4891 atgattatccattttaagttatcatatcaagacgggtattaattttccacgtgataacttttaagagcctgaggggtatttgcattt
1 M I I H L S Y H I K T V L I S H V I T L K S L R V F A F
4975 atacaaatccaaaaacaaaacgtaaatcgttattactttgctatga 5019
29 I Q I Q K Q N V N R Y Y L L *

44AHJDORF047

11911 atgaatgtatgtaagttgttcaggtgtgagttttgcaaaacatttcacagcatagtcataggcttcactatcattcatatcatt
1 M N V C K L F R C E F C K T F H S I V I G F T I I H I I
11995 atctttatcaaaaatcgataattaaaaatctgttttaagttgtga 12039
29 I F I K N R I I K I C F K L *

44AHJDORF045

10655 atggcacccgtcaaagaattgttcacgtacaaaggtttcaaaatcgacgcttgatcaaaggcggttttcggtataccagcagaa
1 M A P S K N C S R T K V S K S T L V S K A F F G I P A E
10739 gcaattttaatctttccattcacttcattatgcattatctttatga 10783
29 A I L I F P F T S Y A Y F L *

44AHJDORF048

15340 atgaggacgttggtgacattatcaatgctggagaagttcaattcacaatttatgaatatgaaaacaaaaagggtcaaaaagggt
1 M R T L L T L S M L E K F N S Q F M N M K T K K V K K V
15256 actcaatcaattttggtcaagtatcatttttaatacaatttcattag 15212
29 T Q S I L V K Y H F N T I S *

44AHJDORF049

5784 atgagggggcaggtgttgactttgatggtgcatatggatttcaatgtatggacttatcagttgcttatgtgtattacattactg
1 M R G Q V L T L M V H M D F N V W T Y Q L L M C I T L L
5868 acggtaaagttcgcatgtgggtaagtctaaagacgcgataa 5909
29 T V K F A C G V M L K T R *

44AHJDORF050

13158 gtgtgttacgtttttcattcacgtaatcgtttcgctgcattttctaaaaaatgtttttgtaaagtccttgatgtattcattttat
1 V C Y V F H S R N R F V A F L K K C F C K V L M Y S F Y
13242 gctttttgtaataaattgtatataatttaaaattggataatatag 13283
29 A F V I N C I Y L N W I I *

44AHJDORF051

11066 atgataacaatgaactatacaatatacattaacggttacaaaaacactgaacgtaatatattattctctacattttgtcacatcac
1 M I T M N Y T I S L T V T K T L N V I Y Y S L H L S H H
10982 gttcattgtataacttattgggttcctttccaataacttaa 10944
29 V H C I T Y W F L S N T *

44AHJDORF052

14338 atgatttttagtaattgttaatttttaatttgatgataaagatttacaaaggcggtacattgacacatggaaacattttgcacatc
1 M I L V M L I L N L M I K I Y K R R T L T H G N I L H I
14254 tgccctatttttctaaagaaagaaacgtatcatatgttaa 14216
29 C P I F L K K E T Y H M *

44AHJDORF053

3348 atgtggttttattcatcaagtgaagttgaaaaatacttacaatcacaagggttcacagaacacaaatgaagatacaacaagtaaca
1 M W F I H Q V K L K N T Y N H K A S Q N T M K I Q Q V T
3432 ctgatgaaacatcgaatcaaaatgctacatcttttag 3467
29 L M K H R I K M L H L *

44AHJDORF054

7551 atgactggaatggaaatcagatgttactcgacgctggtaagatttcacaaaaaactgggtgttaagttacgtacaaaatcaatta
1 M T G M E I R C Y S T L V R F H K K L V L S Y V Q N Q L
7635 ttggttatcataatgaagttcgagtatatccagtag 7670
29 L V I I M K F E Y I Q *

44AHJDORF055

15705 atgtgtctggttaataattcttttgcttggttttggttaaatgatactcgtaagtggttaaaaattctcaatgtattcattat
1 M C L V I I L L L V F W L N D T R E V V K I P Q C I H Y
15789 catcatctaagtaatgaagtataaacctttga 15821
29 H H L S N E V Y N L *

44AHJDORF056

5512 gtgagtattacattacaggttaacaaatggaattatttagagacgcgccagaagaaattaataaaagggtgggtgcatgggttacgtg
1 V S I T L Q V T K W N Y L E T R Q K K L K K W V H G Y V
5596 tgtcaagtggttaacgcagtcggtgaagtaa 5625
29 C Q V V T Q S V K *

44AHJDORF057

10121 atgtaccaccatattgtgcaccatcacgtgtggtattgtatatactcattaatggcggtaccaataatgctgggtgataatattg
1 M Y H H M L H H H V W Y C I H S L M A Y Q I M L V I I L
10205 tattcttttagtggtattgcttaatraa 10231
29 Y S L V V L L N *

SD-138950.1

44AHJDORF058

10767 atgcatatttcttatgattcagtacaaacatcttatctatctgttcgttttcaatatcccatctacctaaggctatcggtcga
1 M H I S Y D S V Q T S Y L S V R F Q Y P I Y L R L S G R
10851 ataaactgggttcaataagggttaa 10877
29 I N W G S I R V *

44AHJDORF164

702 atgttttcatttaattctgttcgtttattttaatcttgaatcttcatatgatgtacccatcatagaacgcgatgtgtttccctca
1 M F S F N S V R L F N L E S S Y D V P I I E R M L F P S
618 tacatgttttaaattcctcctaattctaa 592
29 Y M F K F L L I *

44AHJDORF059

8360 atggattttgtaacattggattacctgaaccgtcattatgccaaaatcttacaccagattctaaaattgcttttaattgttcca
1 M D F V T L D Y L N R H Y A K I L H Q I L K L L L I V P
8276 ttaacatgggtgcgatgtcacgtatag 8250
29 L T W G R C H V *

44AHJDORF060

6257 atgtaccattttcatttctataatattgtgccgtattgggtttcgtttccattttccaaatgtatttacttttgatgtttctaatg
1 M Y H F H F Y N M C R I G F V S I F Q M Y L L L M F L M
6173 ctttgctattactacctgaaaatttag 6147
29 L C Y Y Y L K I *

44AHJDORF061

15551 atgtgttttggtgtcttgataaaatattcttttacgtttgtcattttatttctctcttattttaaattatttgctttctgcaatt
1 M C F G V L I K Y L L R L S F Y F S S Y L N Y L L S A I
15635 gcgattttagttaaattcattgtaa 15658
29 A I C S K S L *

44AHJDORF062

4285 gtggatttcgcaacgcagttaaccaatctattaatattgataaagaacaaatcacatgtactctacacaatccgattctcaaa
1 V V F A T Q L T N L L I L I K K Q I T C T L H N P I L K
4369 aacctgaagggttttggataa 4389
29 N L K V F G *

44AHJDORF063

9487 atgcgtcttgatttttttaataattcttgcgatggcttgttttgctaaagcgagtagtgaactaccactgtcaccactactac
1 M R L V F F L I I L A W L V L L K R V V N Y H C H H Y Y
9403 cactgtcagacgaatcactag 9383
29 H C Q T N H *

44AHJDORF065

5029 gtgggtggaaaacgtttccataatttatatgggtttcttccaacttggtgagtagtgaacactttgaagcattacgcgcaagaggtt
1 V V E N V S I I Y M V S S N L V S M N T L K H Y A Q E V
5113 cacaaaactataaattaa 5130
29 H K T I N *

44AHJDORF064

2609 atgacgagtcaatcaatcaacttgtgtccgaaatatataacgggtgcaccatttgtttaaattgtcacctatgtttaatgcagatg
1 M T S Q S I N L C P K Y I T V H H L L K C H L C L M Q M
2693 acgatatcattgatttaa 2710
29 T I S L I *

44AHJDORF066

10481 atgatattctttatattgaaagtgcacatcggttcattttcacttaacgacttatttccagttgaacgttcagttacataacaaat
1 M I F F I L K V T S V H F H L T T Y F Q L N V Q Y I T N
10397 ctgatttgcataatttaa 10380
29 L I C I Y *